

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run On: December 24, 2002, 16:29:47 ; Search time 1379.08 Seconds  
(without alignments)  
14620.861 Million cell updates/sec

Title: US-09-708-724A-1

Perfect score: 1245

Sequence: 1 atgggaccctggtcagtggt.....ccaggaaagcggtgtagtag 1245

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estnu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_tod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	187.4	15.1	557	17 AQ195794	AQ195794 RPCI11-60
C 2	170.6	13.7	662	17 AG156539	AG156539 Pan trogl
C 3	138.2	11.1	4762	11 BC016151	BC016151 Homo sapi
C 4	137.4	11.0	477	14 BM692143	BM692143 UI-E-CL1-
C 5	131	10.5	331	17 AQ477339	AQ477339 CITBI-E1-
C 6	131	10.5	474	17 AQ476865	AQ476865 CITBI-E1-

C	7	129.4	10.4	455	17	AQ476705	AQ476705 CITBI-E1-
	8	106.8	8.6	367	9	AL709461	AL709461 DKF2p686D
	9	106.8	8.6	816	12	BG540272	BG540272 602569165
	10	106.2	8.5	377	14	T84802	T84802 yd51906.r1
C	11	97.8	7.9	275	12	BF990677	BF990677 RC6-GN007
	12	92.6	7.4	257	12	BF990672	BF990672 RC6-GN007
C	13	87.2	7.0	570	17	B89157	B89157 CIT-HSP-217
	14	86.4	6.9	559	12	BG722262	BG722262 602693433
	15	85.6	6.9	587	17	AQ008399	AQ008399 CIT-HSP-2
	16	85	6.8	360	9	A1274154	A1274154 ql57f09.x
C	17	82.8	6.7	171	14	N45658	N45658 YF77f04.r1
	18	82.2	6.6	470	9	AL982914	AL982914 wz29f09.x
	19	77.8	6.2	488	17	B51476	B51476 CIT978SK-A-
	20	75.6	6.1	285	14	T05398	T05398 EST03287 Fe
	21	74.4	6.0	372	14	U46290	U46290 HSU46290 Hu
	22	74	5.9	845	13	B1561035	B1561035 603254237
	23	70.4	5.7	301	12	BF170089	BF170089 PCL0210 M
	24	70.4	5.7	678	13	B1462516	B1462516 603205421
	25	67.6	5.4	487	9	AA991438	AA991438 os52e04.s
	26	62.4	5.0	392	17	AQ012375	AQ012375 CIT-HSP-2
	27	62.2	5.0	445	17	AQ145842	AQ145842 HS-2218 B
	28	59	4.7	544	12	BG707425	BG707425 602672843
	29	57.2	4.6	413	9	AA021398	AA021398 ze66c08.r
C	30	54.8	4.4	330	10	AW138646	AW138646 UI-H-B11-
C	31	52.2	4.2	844	17	CNS0052P	AL056652 Drosophil
C	32	51	4.1	361	17	AQ379989	AQ379989 RPCI11-16
C	33	51	4.1	378	17	AQ122964	AQ122964 HS-3094 B
C	34	50.2	4.0	734	17	BH839075	BH839075 LMCRI5000
	35	50	4.0	635	17	CNS04A1A	AL281287 Tetraodon
C	36	45.6	3.7	925	17	CNS0091P	AL053013 Drosophil
	37	44.8	3.6	839	17	CNS004NB	AL054280 Drosophil
	38	44.8	3.6	1039	17	AG044494	AG044494 Pan trogl
	39	43.8	3.5	844	17	CNS0052P	AL056652 Drosophil
	40	43.6	3.5	572	13	B1545831	B1545831 603188001
C	41	43.4	3.5	489	17	BH638395	BH638395 1008022C0
	42	43.2	3.5	572	12	BF616922	BF616922 HVSMEC001
	43	43	3.5	925	17	CNS0091P	AL053013 Drosophil
	44	43	3.5	1009	17	CNS010EW	AL098882 Drosophil
	45	42.6	3.4	935	17	CNS006XK	AL066051 Drosophil

#### ALIGNMENTS

RESULT 1  
AQ195794/c  
LOCUS  
DEFINITION  
Drosophila melanogaster, complete genome  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AQ195794 557 bp DNA linear GSS 20-APR-1999  
RPCI11-60I18.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-60I18,  
DNA sequence.  
AQ195794  
AQ195794.1 GI:3607406  
GSS.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 557)  
Adams,M.D., Kounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,  
Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.  
Use of human BAC End Sequences for Sequence-Ready Map Building  
Unpublished (1998)  
Other GSSs: RPCI11-60I18.TK  
Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: mdamas@tigr.org  
Clones are derived from the human BAC library RPCI-11. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from



passed the following selection criteria: Hexamer frequency ORF analysis  
This clone has the following problem: incomplete processing.

#### FEATURES

Location/Qualifiers  
1. 4762  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:313932"  
/tissue\_type="Placenta, choriocarcinoma"  
/clone\_lib="NIH\_MGC\_21"  
/lab\_host="DH10B-R"  
/note="Vector: pOTB7"  
BASE COUNT 1461 a 1022 c 1001 g 1278 t  
ORIGIN

Query Match 11.1%; Score 138.2; DB 11; Length 4762;  
Best Local Similarity 80.9%; Pred. No. 1.2e-24;  
Matches 161; Conservative 0; Mismatches 38; Indels 0; Gaps 0;  
QY 714 TCAATTTGAAGAATCTTTGTCCACCCACACACCACCAAGAAATAATAACAGGA 773  
Db 634 TCTAATCTGAAGATATGTTGTCCACCCACAGCTCCAATTTGAATAATAACAGGA 693  
QY 774 GAGGAGGATGAATTTGGCTCTACCCCTCCAGTAGCAGAACACCTGTACCATC 833  
Db 694 GAGGAGGATGAATTTGACCTATCTCCTCTCCATTTGCAGAACATCTGTACCGCC 753  
QY 834 TCCTTCAGTAACAGAAATGAGACCCCTGCAAGAAATTCGCGGAGCTGTACCATAGC 893  
Db 754 TCCTTTGGTAGCAATAGAACCCCAATACAAAGAAATTTATGCTCTGCTGCCATAGC 813  
QY 894 TGGAGAGCCCTTAGGACAT 912  
Db 814 TGGAGAGCCCTTAGGACCT 832

RESULT 4  
BM692143  
LOCUS BM692143 477 bp mRNA linear EST 28-FEB-2002  
DEFINITION UI-E-CL1-aeo-f-01-0-UI-r1 UI-E-CL1 Homo sapiens cDNA clone  
UI-E-CL1-aeo-f-01-0-UI 5', mRNA sequence.  
ACCESSION BM692143  
VERSION BM692143.1 GI:19005401  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 477)  
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 9704477  
COMMENT Contact: Soares, MB  
Program for Rat Gene Discovery and Mapping  
University of Iowa  
451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: msoares@blue.weeg.uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).  
Seq primer: M13 Reverse.

#### FEATURES

Location/Qualifiers  
1..477  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="UI-E-CL1-aeo-f-01-0-UI"

/clone\_lib="UI-E-CL1"  
/tissue\_type="human retina"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; UI-E-CL1 is a normalized cDNA library containing the following tissue(s): retina. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCGCG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."  
BASE COUNT 147 a 112 c 90 g 128 t  
ORIGIN

Query Match 11.0%; Score 137.4; DB 14; Length 477;  
Best Local Similarity 79.4%; Pred. No. 8e-25;  
Matches 177; Conservative 0; Mismatches 41; Indels 5; Gaps 1;  
QY 707 CTGAATCTCAAAATTTGAAGAATCTTTGTCCACCCACACACCAAGAAATAATA 766  
Db 258 CTGAATCTCAAAATCTGAAGAATATGTTGTCCACCCACAGCTCCAATTTGAATA 317  
QY 767 ACAGAGAGGAGGAGTAATAATTTGGCTGTACCCCTCCAGTAGCAGAACACCTG 826  
Db 318 AACAGA-----GAGGATAAAATTTGGCTGTATACCGCTCTCTCCATTTGAGAACATCTG 372  
QY 827 TACCATCTCTTCAGTAACAGAAATAGACCCCTAGCAATTCGCGGAGCTGCTA 886  
Db 373 TACTGCTCTCTTCAGTAGCAGCAATAGAACCCCAATACAAAGAAATTTTACGCTCTGCTG 432  
QY 887 CCATAGCTGGAGAGCCCTTAGGACATTTGCATTTTCATATTTC 929  
Db 433 TCATAGCTGGAGAGCCCTTAGGACCTTGGCTCTCTCTCTTTC 475

RESULT 5  
AQ477339/c  
LOCUS AQ477339 331 bp DNA linear GSS 23-APR-1999  
DEFINITION CITBI-E1-2582G9.TR CITBI-E1 Homo sapiens genomic clone 2582G9, DNA sequence.  
ACCESSION AQ477339  
VERSION AQ477339.1 GI:4659458  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 331)  
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.  
TITLE Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building  
JOURNAL Unpublished (1997)  
COMMENT Other\_GSSs: CITBI-E1-2582G9.TF  
Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbe@tigr.org  
Clones are available from Research Genetics (info@resgen.com). BAC end search page:  
http://www.tigr.org/tldb/humgen/bac\_end\_search/bac\_end\_search.html.  
Seq primer: M13 Reverse

```
FEATURES
source
Class: BAC ends.
Location/Qualifiers
1. .331
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2582G9"
/sex="male"
/cell_type="sperm"
/notes="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"
BASE COUNT 89 a 66 c 78 g 98 t
ORIGIN
Query Match 10.5%; Score 131; DB 17; Length 331;
Best Local Similarity 88.0%; Pred. No. 3.2e-23;
Matches 154; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

QY 694 CAGGAGCCATGTTCTGAATCTCAAAATTTTGAAGAATCTTTTGTCCACCCACACACCC 753
Db 174 CAGGAGCCATGTTCTGAATCTCAAAATTTTGAAGAATCTTTTGTCCCTCCACACGCGCC 115
QY 754 AAGAAAATAATAACAGGAGGAGGAGGATGAAAATTTGGCGTCTACACCCCTCCAGTA 813
Db 114 ATTG-AAATAATAACAGGAGGAGGAGGATGAAAATTTGGCGTCTACCGCCCTCCAGTA 56
QY 814 GCAGAACACCTGTACCATCTCTTCAGTAACAGAAATAGAGACCCCACTGCAAA 868
Db 55 GTGGACACAGCTGTACTGTCTCTTCAGTAACAGAAATAGAGACCCCAAAACAAA 1

RESULT 7
A0476865/c
LOCUS
DEFINITION
A0476865 474 bp DNA linear GSS 23-APR-1999
CITBI-EI-2581P13.TR CITBI-EI Homo sapiens genomic clone 2581P13,
DNA sequence.
ACCESSION
VERSION A0476865.1 GI:4658984
KEYWORDS
SOURCE
GSS.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 474)
AUTHORS
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE
Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building
JOURNAL
Unpublished (1997)
COMMENT
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1. .474
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2581P13"
/sex="male"
/cell_type="sperm"
/notes="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"
BASE COUNT 127 a 97 c 104 g 139 t 7 others
ORIGIN
Query Match 10.4%; Score 129.4; DB 17; Length 455;
Best Local Similarity 87.4%; Pred. No. 9.4e-23;
Matches 153; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 694 CAGGAGCCATGTTCTGAATCTCAAAATTTTGAAGAATCTTTTGTCCACCCACACACCC 753
Db 174 CAGGAGCCATGTTCTGAATCTCAAAATTTTGAAGAATCTTTTGTCCCTCCACACGCGCC 115
QY 754 AAGAAAATAATAACAGGAGGAGGAGGATGAAAATTTGGCGTCTACACCCCTCCAGTA 813
Db 114 ATTG-AAATAATAACAGGAGGAGGAGGATGAAAATTTGGCGTCTACCGCCCTCCAGTA 56
QY 814 GCAGAACACCTGTACCATCTCTTCAGTAACAGAAATAGAGACCCCACTGCAAA 868
Db 55 GTGGACACAGCTGTACTGTCTCTTCAGTAACAGAAATAGAGACCCCAAAACAAA 1

FEATURES
source
Class: BAC ends.
Location/Qualifiers
1. .455
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2581O9"
/clone_lib="CITBI-EI"
/sex="male"
/cell_type="sperm"
/notes="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"
BASE COUNT 126 a 96 c 100 g 133 t
ORIGIN
Query Match 10.4%; Score 129.4; DB 17; Length 455;
Best Local Similarity 87.4%; Pred. No. 9.4e-23;
Matches 153; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 694 CAGGAGCCATGTTCTGAATCTCAAAATTTTGAAGAATCTTTTGTCCACCCACACACCC 753
Db 174 CAGGAGCCATGTTCTGAATCTCAAAATTTTGAAGAATCTTTTGTCCCTCCACACGCGCC 115
QY 754 AAGAAAATAATAACAGGAGGAGGAGGATGAAAATTTGGCGTCTACACCCCTCCAGTA 813
Db 114 ATTG-AAATAATAACAGGAGGAGGAGGATGAAAATTTGGCGTCTACCGCCCTCCAGTA 56
```







## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
Toshiyuki and Piero Carninci (RIKEN)  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM10739 row: a column: 09  
High quality sequence stop: 559.

## FEATURES

source

Location/Qualifiers  
1..559  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4825616"  
/clone\_lib="NIH\_MGC\_97"  
/lab\_host="DH10B"

/note="Organ: testis; Vector: pBluescriptR (modified  
pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (gtcag  
); Oligo-dT primed using primer 5'-TTTTTTTTTTTWN-3',  
size-selected for average insert size 2.2 kb and  
normalized to R0F 5. This is a primary library enriched  
for full-length clones and constructed using the  
Cap-trapper method (Carninci, in preparation). Library  
constructed by M. Brownstein (NIMH/NHGRI, National  
Institutes of Health). Note: this is a NIH\_MGC Library."

BASE COUNT 93 a 200 c 173 g 93 t  
ORIGIN

Query Match 6.9%; Score 86.4; DB 12; Length 559;  
Best Local Similarity 71.9%; Pred. No. 1.6e-11;  
Matches 141; Conservative 0; Mismatches 51; Indels 4; Gaps 2;  
QY 1054 CAGGACAGAACCATG-AGCCTAGCGAGCGCGGTTCGGAAGCTCCCTCCGCCAAC 1112  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 223 CAGGCCAGAACCATGAACCGCGCGCGCGCGCGCGATGCTCCCTCTCGGCCGAG 282  
QY 1113 GGCGCCTCTCTAGAGCGCTCGG--TGCCCGCCCTCGCGGAGCTGACCCGAGCGCAG 1169  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 283 GTGCGCGCGCGTGCAGTGCCTGTCAGCTTTCAGCGCTGCTGGAGCGCATCCGCGCGAG 342  
QY 1170 TGCAGAGTTGCTCTCTGCGGTGACCGAGGAGGACTGGAGCGCGGATCATCTCCAG 1229  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 343 CAACGAATTGCTCTCTTGGCGCGCGCGGAGGACTGGAGCGCGAGACCTCCCGG 402  
QY 1230 GAAGCGGGCTGAGTAG 1245  
||| |||||  
Db 403 GGACCCAGCGAGGAG 418

## RESULT 15

AQ008399

LOCUS

DEFINITION AQ008399 587 bp DNA linear GSS 27-JUN-1998  
CIT-HSP-2173K13.FR.1 CIT-HSP Homo sapiens genomic clone 2173K13,  
DNA sequence.

ACCESSION

AQ008399

VERSION

AQ008399.1

KEYWORDS

GSS.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 587)

ADAMSON, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden

, K., Berry, K., Granger, D., Suh, E., Wible, C., Kim, U.-J., Shizuya, H.,

Simon, M., and Venter, J.C.

Use of a human BAC End Sequence Database for Sequence-Ready Map

Building

Unpublished (1997)

Other\_GSSs: CIT-HSP-2173K13.TF.1 CIT-HSP-2173K13.TF

CIT-HSP-2173K13.FR

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC

end search page:

[http://www.tigr.org/tldb/hungen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html)

Seq primer: M13 Reverse

Class: BAC ends.

Location/Qualifiers

source

1..587  
/organism="Homo sapiens"  
/db\_xref="GDB:7104311"  
/db\_xref="taxon:9606"  
/clone="2173K13"  
/clone\_lib="CIT-HSP"  
/sex="Male"  
/cell\_type="Sperm"  
/note="Vector: pBelobAC11; Site\_1: HindIII; Site\_2:  
HindIII"

BASE COUNT 115 a 169 c 144 g 159 t

ORIGIN

Query Match 6.9%; Score 85.6; DB 17; Length 587;  
Best Local Similarity 87.0%; Pred. No. 2.6e-11;  
Matches 94; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
QY 931 CCGGCATTCTATCTCTGTCTCAACAAACGAGCGGAGCTGGAGCTGCTGCCG 990  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 361 CCGTCATTTCATCATCTCTGTTCACAAACAGAGTGGCAGCGGAGCTGCTGCCG 420  
QY 991 GAGGTGGAGTGGCTGGCAGAGGGGACATGGCTGCCACCTGCTGCAAG 1038  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 421 GAGGGGAGTGGCTGGCAAGGGGCACACAGCTGCTACCTGCTGCAG 468

Search completed: December 24, 2002, 21:53:37

Job time : 1389.08 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2002, 16:29:47 ; Search time 1107.7 seconds  
(without alignments)  
14620.861 Million cell updates/sec

Title: US-09-708-724A-3\_COPY\_1\_1000

Perfect score: 1000

Sequence: 1 agccagactaggagtgagcc.....cacacatagagtcagagga 1000

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	135.8	13.6	473	9	AL045618
2	86.2	8.6	384	17	AQ277007
3	81.4	8.1	271	17	AQ550173
4	56.6	5.7	883	12	BG719085
5	53.6	5.4	456	17	AQ307435
6	53.6	5.4	874	13	BM453647

7	52.8	5.3	516	17	B17376	B17376 345624.TPB
8	41.6	4.2	735	12	BG722549	BG722549 602694516
9	41	4.1	364	14	BQ261876	BQ261876 f274c09.y
10	39.8	4.0	1086	17	CNS02693	AL181088 Tetraodon
11	39.2	3.9	658	14	BQ263071	BQ263071 f293g02.y
12	39.2	3.9	706	14	BQ262917	BQ262917 f293g02.x
13	38.6	3.9	388	14	C17874	C17874 C17874 Huma
14	37.8	3.8	544	13	BM053816	BM053816 1g42h07.y
15	37.8	3.8	550	13	BM053916	BM053916 1g44b01.y
16	37.8	3.8	603	10	BB636977	BB636977 BB636977
17	37.8	3.8	627	13	B1965182	B1965182 1g34f08.y
18	37.8	3.8	634	12	BF321581	BF321581 uz63c03.y
19	37.8	3.8	664	10	BB666183	BB666183 BB666183
20	37.8	3.8	737	14	BM944288	BM944288 UT-M-EH0p
21	37.8	3.8	942	14	BQ960809	BQ960809 AGENCOURT
22	37.6	3.8	619	14	BQ284460	BQ284460 f290d03.y
23	37.2	3.7	993	17	CNS041BT	AL270002 Tetraodon
24	37	3.7	263	12	BF800030	BF800030 MRI-CI002
25	37	3.7	1011	17	CNS020WT	AL176150 Tetraodon
26	36.8	3.7	844	17	CNS0052P	AL056652 Drosophil
27	36.2	3.6	918	17	CNS04NOA	AL298963 Tetraodon
28	36	3.6	383	10	AV392106	AV392106 AV392106
29	36	3.6	905	17	AZ684627	AZ684627 ENTJX36TF
30	36	3.6	925	17	CNS0091P	AL053013 Drosophil
31	35.8	3.6	450	10	BB730733	BB730733 BB730733
32	35.8	3.6	1016	13	BM543494	BM543494 AGENCOURT
33	35.6	3.6	474	10	BE392622	BE392622 601307451
34	35.6	3.6	536	17	BH313396	BH313396 CH230-101
35	35.6	3.6	728	17	BH271688	BH271688 CH230-34N
36	35.6	3.6	988	17	CNS03P7A	AL254287 Tetraodon
37	35.4	3.5	451	9	AI811650	AI811650 tw44c07.x
38	35.4	3.5	568	12	BF192016	BF192016 243073 MA
39	35.4	3.5	587	12	BF585113	BF585113 602101835
40	35.4	3.5	668	13	BI151722	BI151722 602916278
41	35.4	3.5	818	17	CNS03902	AL234371 Tetraodon
42	35.4	3.5	846	14	BQ734845	BQ734845 AGENCOURT
43	35.4	3.5	1280	13	BM543930	BM543930 AGENCOURT
44	35.2	3.5	497	9	AA562971	AA562971 vl57dl1.r
45	35.2	3.5	532	17	AQ373830	AQ373830 RC111-14

#### ALIGNMENTS

RESULT 1  
AL045618  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AL045618  
473 bp mRNA linear EST 29-FEB-2000  
DKFZp434O035\_r1 434 (synonym: htes3) Homo sapiens cDNA clone  
DKFZp434O035 5', mRNA sequence.

AL045618.1 GI:5433741

EST.  
human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 473)

Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann

,S.

EST (Duesterhoeft, et al.)

Unpublished (1999)

Contact: Duesterhoeft A

MIPS

Am Klopferspitz 18a D-82152 Martinsried, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by Olagen (Hilden/Germany) within the cDNA sequencing

consortium of the German Genome Project.

sl sequence also available.

This clone (DKFZp434O035) is available at the R2PD in Berlin.

Please contact the R2PD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin- Charlottenburg, GERMANY; Email: clone@r2pd.de.

```

FEATURES
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      1. .473
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="DKFZp4340035"
        /clone_lib="434 (synonym: htes3)"
        /tissue_type="testis"
        /dev_stage="adult"
        /lab_host="DH10B"
      /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT 136 a 90 c 148 g 97 t 2 others
ORIGIN
Query Match 13.6%; Score 135.8; DB 9; Length 473;
Best Local Similarity 78.5%; Pred. No. 4.5e-20;
Matches 161; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 525 CACCTCTGAAGCTCCGACGCTCAGGCTTGACACTGAGGCTGACAGGGCCCTTCTG 584
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 268 CCCACACAGACCGCTAGGCTCAGGGCTTGCTACAGTGAAGCTGCGGAGGACCTCGG 327
QY 585 AAGCCAGAGAGATGCCCGGACATAGGCTGAGCAACCTGCTGAGCCAAAGATCT 644
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 328 AAGCAAGGAAGATGCCAAGACACAAAGGCTGAAGCAACCATCTGAGCCAAAGATCT 387
QY 645 GTTTGTCCTCTGATCTTAGTGGCTTCAAAGCGGGTGTGATCAGCCATGGGTAT 704
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 388 GTTTAGTCTCTGATCTCAGCAGCCCTGCCANGAAGGATGATACCATCGGTAN 447
QY 705 CAGACACTGGAGTCCAGTAGCTG 729
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Db 448 CAGACACTGGAGCTGGCAGCTG 472

RESULT 2
AQ277007 384 bp DNA linear GSS 22-NOV-1998
LOCUS CITBI-E1-2515P4.TF CITBI-E1 Homo sapiens genomic clone 2515P4, DNA
DEFINITION
ACCESSION AQ277007
VERSION AQ277007.1 GI:3903203
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 384)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
JOURNAL Unpublished (1998)
COMMENT Other_GSSs: CITBI-E1-2515P4.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
FEATURES
  source
    Location/Qualifiers
      1. .384
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="2515P4"
        /clone_lib="CITBI-E1"
        /sex="male"

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

#### REFERENCE AUTHORS

1 (bases 1 to 1086)  
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.

#### TITLE

Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

#### JOURNAL AUTHORS

2 (bases 1 to 1086)  
Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

#### TITLE

Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

#### JOURNAL AUTHORS

3 (bases 1 to 1086)  
Unpublished  
Genoscope.  
Submitted (12-APR-2000)  
Direct Submission

#### TITLE

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.

#### FEATURES

Location/Qualifiers  
1..1086  
/organism="Tetraodon nigroviridis"  
/db\_xref="taxon:99883"  
/clone="240B09"  
/clone\_lib="G"  
/note="Genoscope sequence ID : COAG240CA05SP1-end : PUC-ori"

BASE COUNT 286 a 222 c 284 g 260 t 34 others  
ORIGIN

Query Match 4.0%; Score 39.8; DB 17; Length 1086;  
Best Local Similarity 53.3%; Pred. No. 96;  
Matches 57; Conservative 11; Mismatches 39; Indels 0; Gaps 0;

QY 888 TGGACACAGCTGGCACTGCTCAACAGAGCCCTACCAAGACATCACTTTTTTTTTTT 947

Db 1022 TTGAACGAGCTTMBCCSCCTTAAAGCGYGCAGAAATCTTTTTTTTTTTTATKTYTC 963

QY 948 TCCACCAACCTGGACCTGAATGGGATGTGGACACACATAGAGTCC 994

Db 962 TCCCCCCCACAGGCCCTCCAGGGGGAGCGGTCCGCCAGRAYTCC 916

#### RESULT 11

BO263071/c 658 bp mRNA linear EST 06-MAY-2002  
LOCUS f239g02.y1 Sugano SJD adult male Danio rerio cDNA clone 5916098 5' similar to TR:Q9WTU0 Q9WTU0 PHD-FINGER PROTEIN. ; mRNA sequence.

#### ACCESSION

BO263071  
VERSION BO263071.1 GI:20463850

#### KEYWORDS

EST.  
zebrafish.

#### SOURCE

Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes ; Cyprinidae; Danio.  
1 (bases 1 to 658)

#### REFERENCE

AUTHORS Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyllie,T., Underwood ,K., Steptoe,M., Theising,B., Allen.M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Willson,R.

#### TITLE

WashU Zebrafish EST Project 1998  
Unpublished (1998)  
Contact: Stephen L. Johnson

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: zbrafish@watson.wustl.edu  
Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA Sequencing by Washington University Genome Sequencing Center Clone Distribution information can be found through the I.M.A.G.E.

Consortium/LINL, send email to: info@image.llnl.gov  
Seq primer: T3 ET from Amersham

High quality sequence stop: 526.

Location/Qualifiers  
1..658

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/organism="Danio rerio"  
/db\_xref="taxon:7955"

/clone="5916098"  
/clone\_lib="Sugano SJD adult male"

/sex="male"  
/tissue\_type="whole body"

/dev\_stage="adult"  
/lab\_host="DH10B (phage resistant)"

/note="vector: pME18S-FL3; Site 1: DraIII (CACCATGTG); Site 2: DraIII (CACTGTGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGCGCCTTTTITTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [GTGTGGCTTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed and donated by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science).

Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAGCTGCG and 3' end primer CGACCTGCAGCTCGACACA."

BASE COUNT 169 a 131 c 173 g 185 t  
ORIGIN

Query Match 3.9%; Score 39.2; DB 14; Length 658;  
Best Local Similarity 62.0%; Pred. No. 1.4e+02;  
Matches 62; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 316 CACTAAATGTTTGGTGGGCTCTTTCTGGAAGCTACCTCTCTCTGTTGGCCCTC 375

Db 393 CACTATAGGGTAATGAAGCCCTCTTTCTCAAGAAGCGTTTGGTCACTGATCCCCCTG 334

QY 376 CATCTTCCCCAACCCAGTACTTCTGGCCATCTCTCTGTC 415

Db 333 CATCTGCACAGATATCCGCTGGCAAGCTCTCTGCCC 294

#### RESULT 12

BO262917 706 bp mRNA linear EST 06-MAY-2002  
LOCUS f239g02.x1 Sugano SJD adult male Danio rerio cDNA clone 5916098 3' similar to TR:Q9WTU0 Q9WTU0 PHD-FINGER PROTEIN. ; mRNA sequence.

#### ACCESSION

BO262917  
VERSION BO262917.1 GI:20463696

#### KEYWORDS

EST.  
zebrafish.

#### SOURCE

Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes ; Cyprinidae; Danio.  
1 (bases 1 to 706)

#### REFERENCE

AUTHORS Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyllie,T., Underwood ,K., Steptoe,M., Theising,B., Allen.M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Willson,R.

#### TITLE

WashU Zebrafish EST Project 1998  
Unpublished (1998)  
Other\_ESTs: fz93g02.y1







GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2002, 16:29:47 ; Search time 1108.8 Seconds  
(without alignments)  
14620.861 Million cell updates/sec

Title: US-09-708-724A-3\_COPY\_50000\_51000  
Perfect score: 1001  
Sequence: 1 agcaacctgtaagtccggc.....ggccctgctgcatgtgacc 1001

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	154.6	15.4	392	12	BF904043
2	135	13.5	331	12	BF901889
3	132	13.2	460	17	AQ478007
4	132	13.2	480	17	AQ198951
5	132	13.2	542	17	AQ630303
6	132	13.2	613	17	AQ427668

7	132	13.2	701	17	AQ473751
8	131	13.1	502	17	AQ692634
9	125.8	12.6	524	17	AQ440312
10	123	12.3	509	17	AQ757386
11	116.2	11.6	430	17	AQ494621
12	110.2	11.0	650	17	AG176043
13	105.2	10.5	393	12	BF901864
14	105.2	10.5	497	17	AQ169608
15	104.8	10.5	578	17	AQ008424
16	103.4	10.3	409	17	AQ674424
17	91.8	9.2	325	17	AQ197958
18	85.8	8.6	456	17	AQ696533
19	85.2	8.5	525	17	AQ784251
20	83.6	8.4	490	17	AQ626785
21	80.4	8.0	404	17	AQ086415
22	80	8.0	330	17	AQ817144
23	79.4	7.9	623	17	AZ521679
24	78.2	7.8	535	17	AQ879443
25	77.2	7.7	501	17	AQ611000
26	69.6	7.0	222	17	B88266
27	61.2	6.1	711	10	BE566324
28	52.4	5.2	669	17	AG034460
29	50.6	5.1	685	17	AQ312269
30	50.4	5.0	718	17	B92472
31	50.2	5.0	689	17	AG184567
32	49	4.9	1007	14	BM806213
33	48.8	4.9	707	17	AQ351078
34	48.4	4.8	1063	14	BM920247
35	47.2	4.7	395	12	BF901989
36	47	4.7	803	14	BM983069
37	46.4	4.6	540	17	AQ756822
38	46.4	4.6	852	17	AQ746055
39	46.2	4.6	663	17	AG089297
40	46	4.6	502	17	AQ155233
41	45.8	4.6	401	17	AQ032208
42	45.6	4.6	366	12	BF901856
43	45.6	4.6	567	17	AQ601940
44	45.4	4.5	440	17	AQ130549
45	45	4.5	752	17	AQ939201

#### ALIGNMENTS

RESULT 1  
BF904043  
LOCUS BF904043 392 bp mRNA linear EST 18-JAN-2001  
DEFINITION IL5-MT0210-201200-338-g09 MT0210 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF904043  
VERSION BF904043.1 GI:12295502  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 392)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R., Negai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001

Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5et3-IL5-MT0210-201200-338-909et3=2000-12-20&ts4=1>  
Seq primer: puc 18 forward  
High quality sequence stop: 382.

FEATURES	SOURCE
1. <b>Feature 1</b>	Source 1
2. <b>Feature 2</b>	Source 2
3. <b>Feature 3</b>	Source 3
4. <b>Feature 4</b>	Source 4
5. <b>Feature 5</b>	Source 5
6. <b>Feature 6</b>	Source 6
7. <b>Feature 7</b>	Source 7
8. <b>Feature 8</b>	Source 8
9. <b>Feature 9</b>	Source 9
10. <b>Feature 10</b>	Source 10
11. <b>Feature 11</b>	Source 11
12. <b>Feature 12</b>	Source 12
13. <b>Feature 13</b>	Source 13
14. <b>Feature 14</b>	Source 14
15. <b>Feature 15</b>	Source 15
16. <b>Feature 16</b>	Source 16
17. <b>Feature 17</b>	Source 17
18. <b>Feature 18</b>	Source 18
19. <b>Feature 19</b>	Source 19
20. <b>Feature 20</b>	Source 20
21. <b>Feature 21</b>	Source 21
22. <b>Feature 22</b>	Source 22
23. <b>Feature 23</b>	Source 23
24. <b>Feature 24</b>	Source 24
25. <b>Feature 25</b>	Source 25
26. <b>Feature 26</b>	Source 26
27. <b>Feature 27</b>	Source 27
28. <b>Feature 28</b>	Source 28
29. <b>Feature 29</b>	Source 29
30. <b>Feature 30</b>	Source 30
31. <b>Feature 31</b>	Source 31
32. <b>Feature 32</b>	Source 32
33. <b>Feature 33</b>	Source 33
34. <b>Feature 34</b>	Source 34
35. <b>Feature 35</b>	Source 35
36. <b>Feature 36</b>	Source 36
37. <b>Feature 37</b>	Source 37
38. <b>Feature 38</b>	Source 38
39. <b>Feature 39</b>	Source 39
40. <b>Feature 40</b>	Source 40
41. <b>Feature 41</b>	Source 41
42. <b>Feature 42</b>	Source 42
43. <b>Feature 43</b>	Source 43
44. <b>Feature 44</b>	Source 44
45. <b>Feature 45</b>	Source 45
46. <b>Feature 46</b>	Source 46
47. <b>Feature 47</b>	Source 47
48. <b>Feature 48</b>	Source 48
49. <b>Feature 49</b>	Source 49
50. <b>Feature 50</b>	Source 50
51. <b>Feature 51</b>	Source 51
52. <b>Feature 52</b>	Source 52
53. <b>Feature 53</b>	Source 53
54. <b>Feature 54</b>	Source 54
55. <b>Feature 55</b>	Source 55
56. <b>Feature 56</b>	Source 56
57. <b>Feature 57</b>	Source 57
58. <b>Feature 58</b>	Source 58
59. <b>Feature 59</b>	Source 59
60. <b>Feature 60</b>	Source 60
61. <b>Feature 61</b>	Source 61
62. <b>Feature 62</b>	Source 62
63. <b>Feature 63</b>	Source 63
64. <b>Feature 64</b>	Source 64
65. <b>Feature 65</b>	Source 65
66. <b>Feature 66</b>	Source 66
67. <b>Feature 67</b>	Source 67
68. <b>Feature 68</b>	Source 68
69. <b>Feature 69</b>	Source 69
70. <b>Feature 70</b>	Source 70
71. <b>Feature 71</b>	Source 71
72. <b>Feature 72</b>	Source 72
73. <b>Feature 73</b>	Source 73
74. <b>Feature 74</b>	Source 74
75. <b>Feature 75</b>	Source 75
76. <b>Feature 76</b>	Source 76
77. <b>Feature 77</b>	Source 77
78. <b>Feature 78</b>	Source 78
79. <b>Feature 79</b>	Source 79
80. <b>Feature 80</b>	Source 80
81. <b>Feature 81</b>	Source 81
82. <b>Feature 82</b>	Source 82
83. <b>Feature 83</b>	Source 83
84. <b>Feature 84</b>	Source 84
85. <b>Feature 85</b>	Source 85
86. <b>Feature 86</b>	Source 86
87. <b>Feature 87</b>	Source 87
88. <b>Feature 88</b>	Source 88
89. <b>Feature 89</b>	Source 89
90. <b>Feature 90</b>	Source 90
91. <b>Feature 91</b>	Source 91
92. <b>Feature 92</b>	Source 92
93. <b>Feature 93</b>	Source 93
94. <b>Feature 94</b>	Source 94
95. <b>Feature 95</b>	Source 95
96. <b>Feature 96</b>	Source 96
97. <b>Feature 97</b>	Source 97
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99. <b>Feature 99</b>	Source 99
100. <b>Feature 100</b>	Source 100

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Mt0210"
/dev_stage="Adult"
/notes="Organ: marrow; Vector:
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,716 - Ludwig Institute for
into the pUC 18 vector. Re
mRNA and cDNA amplification
stringency conditions."
88 a 118 c 111 g 75 t
BASE COUNT
ORIGIN

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Query Match	15.4%	Score	154.6;	DB	12;	Length	392;
Best Local Similarity	68.4%;	Pred. No.	2.2e-35;				
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Gaps	4;						

  

QY	392	GGAGGAAGGTGAGCAGCTGGCGCTGTGCGCTTTGAGGGAGGATGGCGATGTGAAAGTCA	451
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DB	61	GGCCACCCTTTGGCAGGACACTCCCTGGCTCCATCCTCTACATCTTAGGCTTACTGGGAGT	120
QY	512	GTTTGATACACAGAGAAGGAGGAGACCCATCCCAATGGAGGTTTGATTAGATGAATATA	571
DB	121	GTTTGGACACACAGGAGGAGGGGACCTATCCCA--GGAGAAATGGGTAAAGCACTGGA	178
QY	572	ATCAATGATAAATCCCTAGAGAGGGAGCTTTTTATACTCACTCTGAGAACAGGTTGGAG	631
DB	179	ATCAAGACCAATTCCTGACGAGGGGCTGTTTATATCCAACCTCTGAGAACAGGCTG--	235
QY	632	CTACATGGGATTGAGGGGAGGTTGGAGCCCTTTAAAGAAAGACCCACAGAGACTGCCCC	691
DB	236	-----GGGGCGCTGCATGGGACCCCTTCAGAAAATCGCCCAAGGACACAGCCC	283
QY	692	TGCCCTCTCTCCCCACAAAGTTTCAATTTATTTCTTCCACCCAGGAGCTGTCAAGATC	751
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QY	752	CTG--CCCTTCGCTCTCCAGATCAAGATCCCTTCAGGAAATGCAACTACTTC	800
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LOCUS	BF901889
DEFINITION	IL5-MT0210-111200-337-d04 MT0210 Homo sapiens cDNA, mRNA sequence.
ACCESSION	BF901889
VERSION	BF901889.1 GI:12293348
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
CARYOTYPE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
MAMMALIA:	Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE	1 (bases 1 to 331)
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordian,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.T. and

TITLE	Simpson,A.J. Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	200206263
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL ( <a href="http://www.ludwig.org.br/scripts/gethtml2.pl?t1=IL5&amp;t2=IL5-WT0210-111200-337-r04&amp;t3=2000-12-11&amp;t4=1">http://www.ludwig.org.br/scripts/gethtml2.pl?t1=IL5&amp;t2=IL5-WT0210-111200-337-r04&amp;t3=2000-12-11&amp;t4=1</a> )

FEATURES  
SOURCE

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Location/Qualifiers
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/organism="Homo sapiens"
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/dev_stage="Adult"
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Cancer Research) and cloned
into the pUC 18 vector. Re-
sulting cDNA library was
screened for ORESTES cDNA by
mRNA and cDNA amplification
under stringent conditions."
81 a 1102 c 93 q 55 t
BASE COUNT

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Query Match	13.5%	Score 135	DB 12	Length 331
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Qy 512	GTTTGTATACAGAGAAGGAGGAGCACCATCCCAATGGAGGGTTTGATTAGATCAATATA	571		
Db 121	GTTGCACACACACAGGAGGAGGCACTATCCCA--GGAGAAATGGGAAAGCACCTGGA	178		
Qy 572	ATCAATGATAAATTCCTAGAGGAGGGACTTTTTTATACTCAACTCTGAGAACAGGTTG	628		
Db 179	ATCAAGACCAATTCCTGCGAGGAGGGCTGTTATATCCAACTCTGAGAACAGCGTG	235		

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DEFINITION	CITBI-EI-2585E13.TR CITBI-E1 Homo sapiens genomic clone 2585E13, DNA sequence.
ACCESSION	AQ478007
VERSION	AQ478007.1 GI:4660126
KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 460)
REFERENCE	Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
AUTHORS	Use of BAC End Sequences from Caltech Libraries for Sequence-Ready Map Building
TITLE	







Best Local Similarity 64.7%; Pred. No. 1.4e-26; Matches 187; Conservative 0; Mismatches 102; Indels 0; Gaps 0;															
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DB	159	GGTGGTAGTCAGCATGAGAGGGGTGGGGTGGGGTTTATCCATGGGCCACGGGTTTAGT	218												
QY	452	GACCAACCGTGGGAGGACACTCCCTGGGTCCATCCTCTGCATCTTAGATTATTTGGGACA	511												
DB	219	GGATTCCCTGGGACGACACTGCCTGGCTCTATTCTCTTCATCTTAGATGATTGGGGAG	278												
QY	512	GTTTGATACAGAGAAGGAGGAGACCCATCCCAATGGAGGGTTTGATTAGATGAATATA	571												
DB	279	GTATGATACAGAGAAGAGGAGACCCATTTCATTAAGGGTGTGAAATAGGGAACATGA	338												
QY	572	ATCAATGATAAATCTCTAGAGAGGAGCTTTTATATAACTCTGAGAACAGGTTGGAG	631												
DB	339	AATCAAGGACCAATCTTTTCAGGAAGGGTGGCTGTATCTTAACCTCTGAGAACACACT	398												
QY	632	CTACATGGGATTGGAGGGAGGGTGGAGCCCTTAAAGAAAAGCCCA	680												
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RESULT 10															
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LOCUS		HS_5463_B2_E10_T7A		RPCI-11		Human Male		BAC Library							
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ACCESSION		AQ757386													
VERSION		AQ757386.1		GI:5622256											
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ORGANISM		Homo sapiens													
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;													
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.													
TITLE		1 (bases 1 to 509)													
JOURNAL		Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,													
MEDLINE		Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and													
COMMENT		Hood,L.													
TITLE		Sequence-tagged connectors: A sequence approach to mapping and													
JOURNAL		scanning the human genome													
MEDLINE		Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)													
COMMENT		99380589													
TITLE		Contact: Mahairas GG, Wallace JC, Hood L													
JOURNAL		High Throughput Sequencing Center													
MEDLINE		University of Washington													
COMMENT		401 Queen Anne Avenue North, Seattle, WA 98109, USA													
TITLE		Tel: (206) 616-3618													
JOURNAL		Fax: (206) 616-3887													
MEDLINE		Email: jwallace@u.washington.edu													
COMMENT		Clones are derived from the human BAC library RPCI-11. For BAC													
TITLE		library availability, please contact Pieter de Jong													
JOURNAL		(pieter@dejong.med.buffalo.edu). Clones may be purchased from													
MEDLINE		BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)													
COMMENT		or from Resear h Genetics (info@resgen.com). BAC end Web Server:													
TITLE		http://www.htsc.washington.edu													
JOURNAL		Plate: 1039 row: J column: 20													
MEDLINE		Seq primer: T7													
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JOURNAL		Male blood DNA was isolated from one randomly chosen donor													
MEDLINE		and partially digested with a combination of EcoRI and													
COMMENT		EcoRI Methylase. Size selected DNA was cloned into the													
TITLE		pBACe3.6 vector at EcoRI sites"													

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DB	159	GGTGGTAGTCAGCATGAGAGGGGTGGGGTGGGGTTTATCCATGGGCCACGGGTTTAGT	218												
QY	452	GACCAACCGTGGGAGGACACTCCCTGGGTCCATCCTCTGCATCTTAGATTATTTGGGACA	511												
DB	219	GGATTCCCTGGGACGACACTGCCTGGCTCTATTCTCTTCATCTTAGATGATTGGGGAG	278												
QY	512	GTTTGATACAGAGAAGGAGGAGACCCATCCCAATGGAGGGTTTGATTAGATGAATATA	571												
DB	279	GTATGATACAGAGAAGAGGAGACCCATTTCATTAAGGGTGTGAAATAGGGAACATGA	338												
QY	572	ATCAATGATAAATCTCTAGAGAGGAGCTTTTATATAACTCTGAGAACAGGTTGGAG	631												
DB	339	AATCAAGGACCAATCTTTTCAGGAAGGGTGGCTGTATCTTAACCTCTGAGAACACACT	398												
QY	632	CTACATGGGATTGGAGGGAGGGTGGAGCCCTTAAAGAAAAGCCCA	680												
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VERSION		AQ757386.1		GI:5622256											
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SOURCE		human.													
ORGANISM		Homo sapiens													
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;													
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.													
TITLE		1 (bases 1 to 509)													
JOURNAL		Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,													
MEDLINE		Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and													
COMMENT		Hood,L.													
TITLE		Sequence-tagged connectors: A sequence approach to mapping and													
JOURNAL		scanning the human genome													
MEDLINE		Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)													
COMMENT		99380589													
TITLE		Contact: Mahairas GG, Wallace JC, Hood L													
JOURNAL		High Throughput Sequencing Center													
MEDLINE		University of Washington													
COMMENT		401 Queen Anne Avenue North, Seattle, WA 98109, USA													
TITLE		Tel: (206) 616-3618													
JOURNAL		Fax: (206) 616-3887													
MEDLINE		Email: jwallace@u.washington.edu													
COMMENT		Clones are derived from the human BAC library RPCI-11. For BAC													
TITLE		library availability, please contact Pieter de Jong													
JOURNAL		(pieter@dejong.med.buffalo.edu). Clones may be purchased from													
MEDLINE		BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)													
COMMENT		or from Resear h Genetics (info@resgen.com). BAC end Web Server:													
TITLE		http://www.htsc.washington.edu													
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MEDLINE		Seq primer: T7													
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TITLE		High quality sequence stop: 509.													
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JOURNAL		Male blood DNA was isolated from one randomly chosen donor													
MEDLINE		and partially digested with a combination of EcoRI and													
COMMENT		EcoRI Methylase. Size selected DNA was cloned into the													
TITLE		pBACe3.6 vector at EcoRI sites"													

Best Local Similarity 64.7%; Pred. No. 1.4e-26; Matches 187; Conservative 0; Mismatches 102; Indels 0; Gaps 0;															
QY	392	GGAGGAAGGTGAGCAGCTGGCGCTGTGCTTTGAGGGAGGATGGCGATGTGAAAGTCAGT	451												
DB	159	GGTGGTAGTCAGCATGAGAGGGGTGGGGTGGGGTTTATCCATGGGCCACGGGTTTAGT	218												
QY	452	GACCAACCGTGGGAGGACACTCCCTGGGTCCATCCTCTGCATCTTAGATTATTTGGGACA	511												
DB	219	GGATTCCCTGGGACGACACTGCCTGGCTCTATTCTCTTCATCTTAGATGATTGGGGAG	278												
QY	512	GTTTGATACAGAGAAGGAGGAGACCCATCCCAATGGAGGGTTTGATTAGATGAATATA	571												
DB	279	GTATGATACAGAGAAGAGGAGACCCATTTCATTAAGGGTGTGAAATAGGGAACATGA	338												
QY	572	ATCAATGATAAATCTCTAGAGAGGAGCTTTTATATAACTCTGAGAACAGGTTGGAG	631												
DB	339	AATCAAGGACCAATCTTTTCAGGAAGGGTGGCTGTATCTTAACCTCTGAGAACACACT	398												
QY	632	CTACATGGGATTGGAGGGAGGGTGGAGCCCTTAAAGAAAAGCCCA	680												
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DEFINITION		genomic clone		Plate=1039		Col=20		Row=J, DNA sequence.							
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VERSION		AQ757386.1		GI:5622256											
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ORGANISM		Homo sapiens													
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;													
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.													
TITLE		1 (bases 1 to 509)													
JOURNAL		Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,													
MEDLINE		Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and													
COMMENT		Hood,L.													
TITLE		Sequence-tagged connectors: A sequence approach to mapping and													
JOURNAL		scanning the human genome													
MEDLINE		Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)													
COMMENT		99380589													
TITLE		Contact: Mahairas GG, Wallace JC, Hood L													
JOURNAL		High Throughput Sequencing Center													
MEDLINE		University of Washington													
COMMENT		401 Queen Anne Avenue North, Seattle, WA 98109, USA													
TITLE		Tel: (206) 616-3618													
JOURNAL		Fax: (206) 616-3887													
MEDLINE		Email: jwallace@u.washington.edu													
COMMENT		Clones are derived from the human BAC library RPCI-11. For BAC													
TITLE		library availability, please contact Pieter de Jong													
JOURNAL		(pieter@dejong.med.buffalo.edu). Clones may be purchased from													
MEDLINE		BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)													
COMMENT		or from Resear h Genetics (info@resgen.com). BAC end Web Server:													
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TITLE		High quality sequence stop: 509.													
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JOURNAL		Male blood DNA was isolated from one randomly chosen donor													
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TITLE		pBACe3.6 vector at EcoRI sites"													

Best Local Similarity 64.7%; Pred. No. 1.4e-26; Matches 187; Conservative 0; Mismatches 102; Indels 0; Gaps 0;															
QY	392	GGAGGAAGGTGAGCAGCTGGCGCTGTGCTTTGAGGGAGGATGGCGATGTGAAAGTCAGT	451												
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DB	219	GGATTCCCTGGGACGACACTGCCTGGCTCTATTCTCTTCATCTTAGATGATTGGGGAG	278												
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RESULT 10															
AQ757386		AO757386		509 bp		DNA		linear							
LOCUS		HS_5463_B2_E10_T7A		RPCI-11		Human Male		BAC Library							
DEFINITION		genomic clone		Plate=1039		Col=20		Row=J, DNA sequence.							
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VERSION		AQ757386.1		GI:5622256											
KEYWORDS		GSS.													
SOURCE		human.													
ORGANISM		Homo sapiens													
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;													
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.													
TITLE		1 (bases 1 to 509)													
JOURNAL		Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,													
MEDLINE		Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and													
COMMENT		Hood,L.													
TITLE		Sequence-tagged connectors: A sequence approach to mapping and													
JOURNAL		scanning the human genome													
MEDLINE		Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)													
COMMENT		99380589													
TITLE		Contact: Mahairas GG, Wallace JC, Hood L													
JOURNAL		High Throughput Sequencing Center													
MEDLINE		University of Washington													
COMMENT		401 Queen Anne Avenue North, Seattle, WA 98109, USA													
TITLE		Tel: (206) 616-3618													
JOURNAL		Fax: (206) 616-3887													
MEDLINE		Email: jwallace@u.washington.edu													
COMMENT		Clones are derived from the human BAC library RPCI-11. For BAC													
TITLE		library availability, please contact Pieter de Jong													
JOURNAL		(pieter@dejong.med.buffalo.edu). Clones may be purchased from													
MEDLINE		BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)													
COMMENT		or from Resear h Genetics (info@resgen.com). BAC end Web Server:													
TITLE		http://www.htsc.washington.edu													
JOURNAL		Plate: 1039 row: J column: 20													
MEDLINE		Seq primer: T7													
COMMENT		Class: BAC ends													
TITLE		High quality sequence stop: 509.													
JOURNAL		Location/Qualifiers													
MEDLINE		1. .509													
COMMENT		/organism="Homo sapiens"													
TITLE		/db_xref="taxon:9606"													
JOURNAL		/clone="Plate=1039 Col=20 Row=J"													
MEDLINE		/clone_lib="RPCI-11 Human Male BAC Library"													
COMMENT		/sex="male"													
TITLE		/note="Vector: pBACe3.6; Site.1: EcoRI; Site.2: EcoRI;													
JOURNAL		Male blood DNA was isolated from one randomly chosen donor													
MEDLINE		and partially digested with a combination of EcoRI and													
COMMENT		EcoRI Methylase. Size selected DNA was cloned into the													
TITLE		pBACe3.6 vector at EcoRI sites"													

Best Local Similarity 64.7%; Pred. No. 1.4e-26; Matches 187; Conservative 0; Mismatches 102; Indels 0; Gaps 0;									
QY	392	GGAGGAAGGTGAGCAGCTGGCGCTGTGCTTTGAGGGAGGATGGCGATGTGAAAGTCAGT	451						
DB	159	GGTGGTAGTCAGCATGAGAGGGGTGGGGTGGGGTTTATCCATGGGCCACGGGTTTAGT	218						
QY	452	GACCAACCGTGGGAGGACACTCCCTGGGTCCATCCTCTGCATCTTAGATTATTTGGGACA	511						
DB	219	GGATTCCCTGGGACGACACTGCCTGGCTCTATTCTCTTCATCTTAGATGATTGGGGAG	278						
QY	512	GTTTGATACAGAGAAGGAGGAGACCCATCCCAATGGAGGGTTTGATTAGATGAATATA	571						
DB	279	GTATGATACAGAGAAGAGGAGACCCATTTCATTAAGGGTGTGAAATAGGGAACATGA	338						
QY	572	ATCAATGATAAATCTCTAGAGAGGAG							

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BASE COUNT      129 a      97 c      98 g      105 t      1 others
ORIGIN
Query Match      11.6%; Score 116.2; DB 17; Length 430;
Best Local Similarity 78.1%; Pred. No. 9.6e-24;
Matches 139; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 6 CCTTAAGTTTCGGCTGCAATCATAGATAAGTAAGATGGAAGCTTGATGGCAGGGGATG 65
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 34 CCCGCAAAATTCGCTGTATCATACAAAGGAAGCTGGAAGCTTGCTGGCGAGGGATG 93

Qy 66 GCTGAGCTTCATGATAGAAATGTCAGCTTGGGCTGATACATACCACTGGGGGCTC 125
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 94 CTGCACTGTCATGGTAAAAATGACCACTTGGGCCAGACATATACAACTGGGGGCC 153

Qy 126 CACTCCTCTTTGAGCACACCACCATAGGAAGAGTAAGCACTTGGAGTAGCTCA 193
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 154 CNACCCCTCTTGGTACATATGCAGTAGAAGAAAGAGATAAGCACTTGGAGTAGCTCA 211

RESULT 12
AG176043
LOCUS      AG176043          650 bp      DNA      linear      GSS 09-JAN-2002
DEFINITION Pan troglodytes DNA, clone: RP43-047C16.TJ, genomic survey
ACCESSION      AG176043
VERSION      AG176043.1 GI:16705723
KEYWORDS      GSS.
SOURCE      Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
            Male BAC Library clone:RP43-047C16.TJ.
ORGANISM      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE      1
AUTHORS      Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE      BAC end sequences of Library RPCI-43
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 650)
AUTHORS      Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE      Direct Submission
JOURNAL      Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT      Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
            end was generated during the R&D process and may have higher chance
            of clone tracking errors.
PRIMERS
Sequencing: TJ
LIBRARY
Vector      : pBACe3.6
R.Site 1    : EcoRI
R.Site 2    : EcoRI
Location/Qualifiers
1..650
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-047C16.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
BASE COUNT      150 a      162 c      155 g      183 t
ORIGIN
Query Match      11.0%; Score 110.2; DB 17; Length 650;
Best Local Similarity 79.8%; Pred. No. 8.le-22;
Matches 130; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 839 AATTGGGGTTTGGTCCCGATGCCAGTCAAGTGCACAGTCAGATAAAGGTGAGAGCTTA 898
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Db 11 ATTGGGGTTTTTGGTCCCGTCTCTGAAGTGTGCACAGTCAGATAAAGGTGAGGGCCTA 70
Qy 899 GGAGATTAGCGGAGGAGTAGAAGAACACTCTCTGTGTACACAGCTTCAGAGAGCTGGGG 958
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 71 ACAGATTAGCAGATGGTAGGAAGACTCTATCTTGCAGCCAGCTTCAGAGAGCTGTGG 130
Qy 959 CCATGGCTTTCCTGCTCAACATTAGGCCCTCTGCTGCATGGTGACC 1001
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 131 CCATGGCTCCCGAGTCAACATTAGGCCCTGTGCTGGGAACC 173

RESULT 13
BF901864
LOCUS      BF901864          393 bp      mRNA      linear      EST 18-JAN-2001
DEFINITION IL5-WT0210-111200-337-h09 MT0210 Homo sapiens cDNA, mRNA sequence.
ACCESSION      BF901864
VERSION      BF901864.1 GI:12293323
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 393)
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE      Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
COMMENT      Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5et2-IL5-WT0210-
            111200-337-h09et3-2000-12-11et4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 392.
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            /organism="Homo sapiens"
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            /clone_lib="MT0210"
            /dev_stage="Adult"
            /note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
            SmaI; A mini-library was made by cloning products derived
            from ORESTES PCR (U.S. Letters Patent application No. 196
            716 - Ludwig Institute for Cancer Research) profiles
            into the pUC 18 vector. Reverse transcription of tissue
            mRNA and cDNA amplification were performed under low
            stringency conditions."
BASE COUNT      97 a      115 c      98 g      83 t
ORIGIN
Query Match      10.5%; Score 105.2; DB 12; Length 393;
Best Local Similarity 62.4%; Pred. No. 1.9e-20;
Matches 257; Conservative 0; Mismatches 133; Indels 22; Gaps 5;

Qy 468 ACATCTCCCTGGCTCCATCTCTGCATCTTAGATTATTGGGACAGTTGTATACACAGA 527
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ACATCTCGGTGATCCATCTCTACATCGTAGGCTTACTGGAGTGTGTGACACACAGG 60
Qy 528 AGGAGGAGACCCATCCCAATGGAGGGTTTGATTAGATGAATATATCAATCAATAATTC 587
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 61 AGGAGGGACCTATCCCA--GGAGAAAATGGGAAAGCACTGGGAATCAAGACCAATTC 118
Qy 588 TAGAGAGGGAGCTTTTATATCAACTCTGAGACAGGTTGGAGCTACATGGGATTGGAG 647
Db 119 TCCAGGAGGGGCTGTTATATCCAACTCTGAGACAGGCTG-----GGGG 163
Qy 648 GGGAGGGTGGAGCCCTTAAAGAAAGAACGCCAGAGACTGCCCTGCCCTCTCTCTCCCC 707
Db 164 CGCTGATGGGACCCCTTCAGAAAATGCCCCAGGACAGCCC--CTTCTCCCTGCGCTG 221
Qy 708 CACAGTTCCTATTTATATCTCCACCCAGGAGCTGTCCAGATCCTG--CCCTCCGCT 765
Db 222 CCAAGAGGCCCCCAAGCACTTCACCCAGGCCCTGTCCAGCATCTGCTCTGTCTCTA 281
Qy 766 CCAGATCAAAAGTCCTTCAGGAAATGCAACTACTTC-AGTGACAAGAGATAATTAATCATCT 824
Db 282 GGAGTCCGAGTTCTGACAGGAATGACAGCTGCTCCAAGTGGCTGCCATGAATTACAGCT 341
Qy 825 TCTGACAGGAGGAATTTGGGGTTTGTCCAGTCCCATGGAAGTGGCACAGT 876
Db 342 TCGTCTCTTGAGAAATTTGTCACTATTTCCAAAGAATGGAGCAGCTCAGT 393

RESULT 14
LOCUS AQ169608 497 bp DNA linear GSS 16-OCT-1998
DEFINITION HS_3176_B2_G12_T7 CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3176 Col=24 Row=N, DNA sequence.
ACCESSION AQ169608
VERSION AQ169608.1 GI:3567283
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 497)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3176 row: N column: 24
Class: BAC ends
High quality sequence stop: 497.
FEATURES
source
Location/Qualifiers
1..497
/organism="Homo sapiens"
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
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BASE COUNT 114 a 153 c 82 g 148 t
ORIGIN
Query Match 10.5%; Score 105.2; DB 17; Length 497;
Best Local Similarity 84.9%; Pred. No. 2.2e-20;
Matches 141; Conservative 0; Mismatches 23; Indels 2; Gaps 2;

Qy 17 GGGCTGCAATCATACATAGTAAGTGAAGCTTCTATGGCC-AGGGATGGCTGCAGCTT 75
Db 48 GTGCTGCAATCATACAAAAGGAAGCTTGTGTGGGCTAGGATGCTGCAGCTG 107

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Qy 76 CATGATAGAAAATGTCAGCTTGGCTAGATACATCAACAT--GGGGGCTCCACTCTCT 134
Db 108 CATGGTAGAAATGACCACCTTGGCCAGACATATCAACATGGGGGCCCCACCTCT 167
Qy 135 TTGTAGCACAGCCACCATAGGAAAGAGATAAGCAACTTGGAGTAGC 180
Db 168 TTGTAGCATAGCCACAGTATATAAAGAGATAAGCACCTTGGAGTATC 213

RESULT 15
LOCUS AQ008424 578 bp DNA linear GSS 27-JUN-1998
DEFINITION CIT-HFP-2062M17.TF CIT-HSP Homo sapiens genomic clone 2062M17, DNA
sequence.
ACCESSION AQ008424
VERSION AQ008424.1 GI:3128531
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 578)
AUTHORS Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden
,K., Berry,K., Granger,D., Suh,E., Wible,C., Kim,U.-J., Shizuya,H.,
Simon,M. and Venter,J.C.
TITLE Use of a human BAC End Sequence Database for Sequence-Ready Map
Building
JOURNAL Unpublished (1997)
COMMENT Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21;
Class: BAC ends.
FEATURES
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="2062M17"
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/sex="Male"
/cell_type="Sperm"
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HindIII"
BASE COUNT 148 a 146 c 129 g 155 t
ORIGIN
Query Match 10.5%; Score 104.8; DB 17; Length 578;
Best Local Similarity 87.5%; Pred. No. 3.2e-20;
Matches 126; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

Qy 41 ATGGAAGCTTGTATGGGAGGATGGCTGCAGCTTCATGTAGATAAGATGCCAGCTTGGG 100
Db 43 ATGCAAGCTTGTGGGAGGATGCCCTGCAGCTGCATGGGTAGAAATGACCACTTGGG 102
Qy 101 CTAGATACATCAACAT--GGGGGCTCCACTCTCTTTTGTAGCACAGCAGCATAGGAAAG 159
Db 103 CCAGACATATCCACATGGGGGGCCCCACCTCTTTTGTAGCATATGCACATAGAAAG 162
Qy 160 AGATAAGCAACTTGGAGTAGCTCA 183
Db 163 AGATAAGCAACTTGGAGTAGCTCA 186

Search completed: December 24, 2002, 21:54:01

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Job time : 1115.8 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2002, 16:29:47 ; Search time 1108.8 Seconds  
(without alignments)  
14620.861 Million cell updates/sec

Title: US-09-708-724a-3\_COPY\_70000\_71000

Perfect score: 1001

Sequence: 1 ggagatggataaacccgtgtg.....ccaatcaggagctatgtg 1001

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16134066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estnu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_estli:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_mus:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	522.2	52.2	640	12	BG534918 602554106
C 2	418.6	41.8	808	9	AU136659 AU136659
C 3	357.8	35.7	649	10	BE150830 BE150830
C 4	307.6	30.7	524	12	BG003846 MR3-GN018
C 5	299	29.9	507	12	BF879658 RC2-ET018
C 6	281.8	28.2	500	12	BF879654 RC2-ET018

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

7	280.6	28.0	625	13	BI046524
8	272	27.2	464	13	BI057039
9	250.6	25.0	658	10	AV721454
10	248.2	24.8	743	17	AG183922
11	237.2	23.7	574	12	BG777821
12	223.8	22.4	636	17	AQ00691
13	217.8	21.8	418	9	AI830956
14	217.8	21.8	524	12	BF725513
15	217.8	21.8	576	13	BI115904
16	217.8	21.8	579	10	BE263504
17	217.8	21.8	591	10	BE258753
18	217.8	21.8	598	12	BG716902
19	217.8	21.8	693	13	BI547646
20	217.8	21.8	702	12	BE795896
21	217.8	21.8	709	12	BG705551
22	217.8	21.8	738	13	BI767440
23	217.8	21.8	810	12	BG764162
24	217.8	21.8	820	14	BM725035
25	217.8	21.8	838	14	BQ217512
26	217.8	21.8	861	13	BI916025
27	217.8	21.8	881	14	BQ224422
28	217.8	21.8	888	13	BI547711
29	217.8	21.8	908	13	BQ684259
30	217.8	21.8	916	13	BI757276
31	217.8	21.8	918	12	BG760309
32	217.8	21.8	977	12	BG395462
33	217.8	21.8	978	14	BQ683756
34	217.8	21.8	1008	13	BM475273
35	217.8	21.8	1019	13	BM468970
36	217.8	21.8	1079	14	BM800060
37	217.8	21.8	1094	14	BM811369
38	217.4	21.7	511	10	AW162774
39	217	21.7	803	12	BG431001
40	217	21.7	1081	12	BE907415
41	216.8	21.7	354	13	BI057453
42	216.2	21.6	417	10	AW370537
43	215	21.5	446	9	AA988929
44	214	21.4	627	10	AV647395
45	210.2	21.0	430	10	AW104316

## ALIGNMENTS

RESULT 1	BG534918/c	BG534918	640 bp	mRNA	linear	EST 03-APR-2001
LOCUS	602554106f1 NIH_MGC_77	Homo sapiens	cdna clone	IMAGE:4663824 5',		
DEFINITION	mRNA sequence.					
ACCESSION	BG534918	GI:13526461				
VERSION	BG534918.1					
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	1 (bases 1 to 640)					
TITLE	NIH-MGC http://mgc.nci.nih.gov/.					
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)					
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaphs-r@mail.nih.gov Tissue Procurement: CLONTECH Laboratories, Inc. CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCMI466 row: 1 column: 01 High quality sequence stop: 639.					
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/db_xref="taxon:9606"
/clone="IMAGE:4663824"
/clone_lib="NIH_MGC_77"
/lab_host="DH10B (TI phage-resistant)"
/notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgctcgccg); Site_2: SfiI (ggcgctatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGCGGCGGACATG-dh(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
BASE COUNT      170 a 134 c 166 g 170 t
ORIGIN
Query Match      52.2%; Score 522.2; DB 12; Length 640;
Best Local Similarity 90.6%; Pred. No. 7e-152;
Matches 579; Conservative 0; Mismatches 58; Indels 2; Gaps 2;
QY 210 CAGAGCTGAGAAACTGGTGTAGTGCCAGGTCAGGCAAAACCCCTGACCTCCATGTTA 269
Db 638 CAGGAATTGAAAAATGCTGGAGCGCAGGCTCAGGGGAAAAACCCAGACTCCATGTTA 579
QY 270 TGGCCATGCTAGC-TGTAAATATCTGTGCAGTATGATTTTCTGTGCAGAGCAAAACA 328
Db 578 TGGCCATGCTAGCTGTAATATCTGTGAGGTATGTTTCTCCTGTGCAGAGC-AATACA 520
QY 329 TATTGGGCATATTTCTTAACCCACCGGTAGTGTGATCATCTCTGAAGCAGCCTCCTC 388
Db 519 TATTGGGCATATGTTCTTAACCCACTGCTAGTGTGACCATACTCTGGAACGACACTCCTC 460
QY 389 CTGAGATATATCATGATCAAGAGCATCAGTACCAGGACCTCTAACTCCCTCCACAG 448
Db 459 CTGAGATATATCATGATCAAGGACATAGGCACGACCCCTTAATCTCCCTGCACAG 400
QY 449 AGCAATTAGACTCTCAATAACAAATGATATCAATATACACATCCATTTGGAGGACTTCCTT 508
Db 399 AGCAATTAGACTCTCAGNACAATGGTATCAATATACACATCCATTTGGAGGAACTTCCTT 340
QY 509 TATGTGCACCCAGATATGCTCAACTGCAGTTGCTTGCAGTTTGATTTGATCCCAAGCAT 568
Db 339 TATGGCTCACCCAGGATACCTCACTCACTCACTTGCCTTGCATTTCAATTCCTCAAGCAT 280
QY 569 GGTGTAGTTACCAATAAAAAATATGTACCTATTAGACCTTTAGCTTTATTAATATTACTT 628
Db 279 GGCTGAGTTACCATGGAATATATTATGACCTATTAGGCTTTAGCTTCTATTATTACTG 220
QY 629 GTGTAGTTACTAATCACTCTCGGCCCATCACCAAAATTTGACTATTATACAAATGGG 688
Db 219 GTGTGTTTACTAATCACTCTCGGCCCATCGCCCAAAATTTGATTATATACAAATGGG 160
QY 689 CTCCCTTTGATAATCTCACCCCTCTCTGGGCCACTGCTTGGCCCTTTAGCTAGAC 748
Db 159 CTCCCTTTGATAATCTCACCCCTCTCTGGGCCACTGCTTGGCCCTTTAGCTAGAC 100
QY 749 AATAGTCCATCTTAATGGGACATATTATTGACTGGGGTCCCTGTGGTCATTAAAGATGGG 808
Db 99 AACAGTCCATCTTAATGGGACATATTATTGACTGGGGTCCCTGTGGTCATTAAAGATGGG 40
QY 809 GAGATGAGATACAGACCATGGGATCAAACTTCACCTGCG 847
Db 39 GAGATGAGATACAGACCTCAGGCATAGCTTCTACTAGC 1
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RESULT 2
AUI36659
LOCUS
DEFINITION AUI36659 PLACE1 Homo sapiens cdna clone PLACE1004793 5', mRNA
ACCESSION AUI36659
sequence.
AUI36659
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VERSION AUI36659.1 GI:10997198
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 808)
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Tsugai,T.
TITLE HRI human cdna project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cdna project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cdna library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
source Location/Qualifiers
1..808
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PLACE1004793"
/clone_lib="PLACE1"
/tissue_type="placenta"
/notes="Vector: pME18SFL3"
BASE COUNT 227 a 186 c 169 g 219 t 7 others
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Query Match 41.8%; Score 418.6; DB 9; Length 808;
Best Local Similarity 76.1%; Pred. No. 2.2e-119;
Matches 553; Conservative 0; Mismatches 171; Indels 3; Gaps 3;
QY 257 GACTCCATGTTTATGGCCATGCTAGCTGTATATATCCCTGTGCAGTATGATTTTCTGTGCA 316
Db 1 GATTCCTGTTCTTGGCCATGTTAGCCATATATATCCCTGTGCAGTATGTTTCTGTGCA 60
QY 317 GAAGCAAAACATATTTGGGCATATTTTCTTAACCCACGGTAGTGTGA-TCATACTCTGA 375
Db 61 GAGCAAAACATATTTGGGCATATGTTCCCAAGCCCCAGCAGTATGACCCATACTTTGG 120
QY 376 AGCAGCACTCTCTCTGAGATATATCATGATCAAGGAGCATCAGTACCAGGACCTCTAACT 435
Db 121 AGTCACTCTCTCTAGATTTATCATGATTTAGGAGCATGGGCTCCAGGACCCCTAACT 180
QY 436 CCCCTGACAGAGCAATTAGACTCTCATAAATGGTATCAATATPACACATCCATTG 495
Db 181 CCACCTGACATAGAACAGTTAGACTCTCAGAATAATGTGCTAATATATACCGCTCCATTG 240
QY 496 GAGGACTTCCTTTATGTGTCACCCAGGATACATGCTCAACTGCAGTTGCCCTTGCAGTT 555
Db 241 GAAGGACTTCCTTTGTGTGTACCAACAAAGACATCACTCAGCCCATAGCTGCTTTACAGTT 300
QY 556 TGATCCCAAGCATGGTTGAGTTACCATAAAAAATTTATGTACCTATTAGACCTTAGCTTTT 615
Db 301 CAAGCTCACATGTTGAGTCATCTATGGGAAATCATGTACTTATTAACTCTTGGTTAT 360
QY 616 ATTAATATTACTTGTGTAGTTTACTTAATCACTCTCGGCCCATCACCCAAATTTAGTGTAT 675
Db 361 ATTAATGTAACCGGTGTGCTAAACCAACCATTCCTGGCCCAATCGCTTCATTTGCTGAC 420
QY 676 TATACAGAAATGGGCTCCCTTTTGATAATTTCTCACCCCTCTCTGGGCCACTGCTTTGGC 735
Db 421 TATACAGAAATGGATTCCTTCAATAGTTTCTTACCCCTCCATAGACCCAGTCTTGGC 480
QY 736 CCCTTAGTACACAAATAGTCCATGTTAATGGGAGACATATTGACTGGGGTCCCTGTGTGT 795
Db 481 CCATGGCTAGAAAAACAATCTATGTTAACTGGAGACATTTGGATTGGGGACCTAAAGGC 540
```



Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR3&t2=MR3-GN0187-201100-011-e04&t3=2000-11-20&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 5  
High quality sequence stop: 524.  
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/db\_xref="taxon:9606"  
/clone\_lib="GN0187"  
/dev\_stage="Adult"  
/note="Organ: placenta\_normal; Vector: puc18; Site\_1: SmaI  
; Site\_2: SmaI; A mini-library was made by cloning  
products derived from ORESTES PCR (U.S. Letters Patent  
application No. 196,716 - Ludwig Institute for Cancer  
Research) profiles into the pUC 18 vector. Reverse  
transcription of tissue mRNA and cDNA amplification were  
performed under low stringency conditions."  
142 a 135 c 140 g 107 t

FEATURES  
source  
Query Match 30.7%; Score 307.6; DB 12; Length 524;  
Best Local Similarity 83.6%; Pred. No. 9.5e-85;  
Matches 378; Conservative 0; Mismatches 59; Indels 15; Gaps 2;

Qy 1 GGAGATGATAAACCGTGTGAGTGGCCCTCAAGTTGTGTGCGACCATGGAATGGGAGACTG 60  
Db 85 GGAGATGACAATCCGTGTGGTGGCCCTCAAGTTGTGTGCGACCATGGAACGGGAGACTG 144  
Qy 61 GAGGATACATGGATCCCACTACAGGCCCGCCAGCTCCTCCAGTATGAGCCATGAGCCAGTT 120  
Db 145 GAGAAATCCATGGATCTCAACTGTGGGCCCGCCAGCTCCTCCAGTACGAGCCATGAGCTAGTT 204  
Qy 121 GAATCTGAATGTGAAGATGAATGAAGACGACGAGAGCTACACTGAGCTCAACCCCTCAT 180  
Db 205 GAATCTGAATGCAAGACAGACAGACAGACAGGACCGGAGTCACTGACATCAACCCCAT 264  
Qy 181 AACATGGGGTGCAGATCAAGAAACACACACAGAGCTGAGAACTGGTGTAGTGCCAGGG 240  
Db 265 AAAAGGGGACAGCTCAAGAAACACACACAGAGCTGAGAACTGCTGGAG----- 316  
Qy 241 TCAGCAAAACCCCTGACTCCATGTTTATGGCCATGCTAGCTGTATATCTGTGCACT 300  
Db 317 -----CAAAACCCCTGACTCCATGTTTATGGCCATGCTAGCTGTATATCTGTGCGGT 370  
Qy 301 ATGATTTTCTGTGCAGAGCAAAACATATTGGGCATATTTCCTAACCCACCGGTAGT 360  
Db 371 ATGTTTCCCTGTGCAGAGGCAAAACATTATTGGGCATATATTCCTAACCCACCGTAGT 430  
Qy 361 GTGATC- ATACTCTGAAGACGACCTCCTCCTGAGATATATCATGATCAAGGAGCATCAGT 419  
Db 431 ACGACCGTACTCTGGGAGCAACACTCCTCCTGAGATATATCATGATCAGGAGCATGGAC 490  
Qy 420 ACCAGGACCTCTAATCCCTCCCTGCACAGAG 451  
Db 491 ACCAGGACCCCTAATCCCTCCCTGCACAGAGAG 522

RESULT 5  
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LOCUS BF879658  
DEFINITION RC2-ET0188-271100-011-e04 ET0188 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF879658  
VERSION BF879658.1 GI:12269788  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 507)  
Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC2&t2=RC2-ET0188-  
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High quality sequence start: 12  
High quality sequence stop: 507.  
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/clone\_lib="ET0188"  
/dev\_stage="Adult"  
/note="Organ: lung\_tumor; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
136 a 110 c 132 g 129 t

BASE COUNT  
ORIGIN  
Query Match 29.9%; Score 299; DB 12; Length 507;  
Best Local Similarity 81.4%; Pred. No. 4.6e-82;  
Matches 372; Conservative 0; Mismatches 80; Indels 5; Gaps 2;

Qy 547 CTTGCAGTTTGATCCCAAGCATGGTTGAGTTACCATATAAAATATGTACCTATTAGAC 606  
Db 506 CTTGCAGTCCAATCTCAGGCATGGTTAAGTCAATGAAATATGATTTATTAGC 447  
Qy 607 CTTAGCTTTATATATATCTGTGTAGTTACTACTCTCTCGCCCATCACCCTCAAT 666  
Db 446 CTCAGCTTTATTAAGTTACTTGGCGGTGTCAACATCACTCCAGCCCTCTCTTGACTCAAT 387  
Qy 667 TGTACTGATTATACAGATGGCTCCCTTTGATAATTCTACCCCTCTCTTGGGCCCC 726  
Db 386 TGTATGATTATATGAATGGCTCCCTTTGATATTCTACCCCTCTCTTGACTCAG 327  
Qy 727 TGTCTTGGCCCTTAGCTAGACAATAGTCCATGTTAATGGGAGACATTTTACTGGGT 786  
Db 326 TGTCTTGGCCCTTGGCCAGACACAGTCTATGTTAATGGGAAC---ATTGACTGGGT 270  
Qy 787 CCCTGTGTCTATTAGATGGGAGAGATGAGATCAGACCATGATGATATAACTTCACTGG 846  
Db 269 CCCGTTGCCATTTAGAGGGGAGAGATGAATCAGACCTCTTGGCACAACACTTCACTGG 210  
Qy 847 CACTGGTGGCGAAACTTTAATCATCTCTTCACTTCAACACACTGGGATTCAAT--CCCAAT 904  
Db 209 CACTGGTGGTGGACCTTCAACACCTCTTCAATCATCATCATCATGGGATTCACTCCCCAGT 150  
Qy 905 CTGCCATGCAACTTGTGTTGGCATGGAAGGGCTTTAGCCCACTTTGCTCTCAATGGCAT 964



performed under low stringency conditions."

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BASE COUNT      168 a   153 c   169 g   135 t
ORIGIN

Query Match      28.0%; Score 280.6; DB 13; Length 625;
Best Local Similarity 75.5%; Pred. No. 3e-76;
Matches 422; Conservative 0; Mismatches 114; Indels 23; Gaps 5;

QY 1 GGAGATGGATAAACCGTGTGAGTGGCCCTCAAGTCTGTGCGACCACTGGAATGGGAGACTG 60
DQ 1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 47 GGAGATGGACAACCGTGTGGTGGCCCTCCAGTGTGTGTGACCATGGAACGGGAGACCG 106
QY 61 GAGGATACATGGATGCCAACATACAGGCCAGCTCCTCCAGTATGAGCATGAGCCAGTT 120
DQ 61 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 107 GAGGATCCATGGTATTCAACCGTGGGCTGTACCTCCAGTACGAGCATGAGCCAGCG 166
QY 121 GAATCTGAATGTGAAGTGAATGAAGACCGAGAGAGATGACATGACATCAACCTCAT 180
DQ 121 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 167 GAATCTGAATGCAAGACAGACAAGGCGCGACCGAGGTCACAATGACATCCAAACCCAT 226
QY 181 AACATGGGTGAGATCAAGAAACACACAGAAAGCTGAGAACTGGTGTAGTGCCAGGG 240
DQ 181 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 227 AACATGGGACAGATCAAGAAACACACAGAAAGCTGAGAACTGAGTACGAGCGCCAGG 286
QY 241 TCAGCAAAAACCCCTGACTCCTCATGTTATATGCCATGCTAGCTGA-ATATCCTGTGCAG 299
DQ 241 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 287 TCAGGCAAAAACCCCTGACTCCTCATGTTCTTGGCCATGCTAGCTAGTTGCTCTGGCG 346
QY 300 TATGATTTTCTG-TGCAGAACAAAACATATTTGGCATATTTTCTTAACCCACCGTA 358
DQ 300 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 347 TATGTTTCCCTGTGTAGAGCAAAAACATATTTGGCATATTTTCTTAACCCACCGTA 406
QY 359 GTGTGATCA- ---TACTCTGGAAGCAGCACTCCTCTCGAGATATATCATGATCAAGGACGA 414
DQ 359 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 407 GTAGTACGACTGTACTCTGGAGCAGACTCCTCTCGAGATATATGATCAGGAGCG 466
QY 415 TCAGTACCAGGACCTTAACTCCCTGACACAGAGCAATTAAGCTCTCAATCAATGGT 474
DQ 415 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 467 T-GGGACCAGGAACCTAACTCCGTCTGACACAGAAATGATCATCAATATACACGGG- 523
QY 475 ATCAATTATACACATTCATTTGAGGAGCTTCTTTATGTGTGTCACCCAGGATACATGCTC 534
DQ 475 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 524 -----CCCATGTGAAGGACTCCCTTTATTGTTCCACCATGATACGTCACCTC 569
QY 535 AACTGCAGTTGCTGTGCAG 553
DQ 535 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 570 AACTGCAGCTGTCTTGCAG 588

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DEFINITION PM2-GN0500-220201-002-b12 GN0500 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BI057039
VERSION     BI057039.1  GI:14464569
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 464)
AUTHORS    Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE      Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE    20202663
COMMENT    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
```

```
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM2&t2=PM2-GN0500-
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                /note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI
                ; Site_2: SmaI; A mini-library was made by cloning
                products derived from ORESTES PCR (U.S. Letters Patent
                application No. 196,716 - Ludwig Institute for Cancer
                Research) profiles into the puc 18 vector. Reverse
                transcription of tissue mRNA and cDNA amplification were
                performed under low stringency conditions."
BASE COUNT      112 a   122 c   101 g   129 t
ORIGIN

Query Match      27.2%; Score 272; DB 13; Length 464;
Best Local Similarity 80.5%; Pred. No. 1.2e-73;
Matches 356; Conservative 0; Mismatches 80; Indels 6; Gaps 3;

QY 536 ACATTGCTCAACTGCAGTTGCTTCAGT-TTGATCCCAAGCATGTTGAGTTACCATAA 584
DQ 536 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 20 AGCTCACTCACTGCAGCTGCTTGAGGTCCAAATCTCAGGCATGTTAAGTCACCATGG 79
QY 585 AAAAATTATGACCTATTAGACCTTAGCTTTATTAATATTACTTTGTAGTTACTTAATCA 644
DQ 585 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 80 AAAAATTATGATTTATTAGGCTCAGCTTTATTAATGTTACTGCGTGTTCACCAATCA 139
QY 645 CTCCTGGGCCCATCAACCAAAATTGACTGATATACAGAAATGGGCTCCCTTTGATAATTC 704
DQ 645 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 140 CTCCTGGGCCCATCACTCAAAATGATGATATATATGAATGGGCTCCCTTTGATAATTC 199
QY 705 TCACCCCTCTCTGGGCCCACTGCTTGGCCCTTAGTCAGACAAATAGTCATCTTAAT 764
DQ 705 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 200 TCACCCCTCTCTGGGACTGCTTGGACCTTGGCCCAACACAGTCTATGTTTAAAT 259
QY 765 GGGAGACATTATTGACTGGGTCCCTGCTGATTAAGATGGGAGAGATGAGAATCAGAC 824
DQ 765 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 260 GGGAAAC- --ATTGACTGGGTCCCGTGGCCATTTAGAGGGGAGAGATGAAATCAGAC 316
QY 825 CACATGGCATAACTTCACTGCGACTGTGGGAAACTTTTAACATCTCTTCACTTCAACA 884
DQ 825 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 317 CTCCTGGCAAAACTTCACTGCGACTGTGGTGGGACTTCAACACCTCTTCACTCAATCA 376
QY 885 CACTGGGATTCAAAT-CCCAATCTGCCATGCAACTTGTGTCATGGAACGGCTTTAGC 942
DQ 885 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 377 CACTGGGATTCAGTCCCGCAGTGGCTGCAACAACCTTGTGTTATAGGACAGGCTTTAAC 436
QY 943 CCACCTTTGCCCTCAATGGCATT 964
DQ 943 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 437 CCGCCCTTACCTCAGTGACGTT 458

RESULT 9
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LOCUS      AV721454      658 bp      mRNA      linear      EST 16-OCT-2000
DEFINITION AV721454 HTB Homo sapiens cDNA clone HTBAKH02 5', mRNA sequence.
ACCESSION  AV721454
VERSION     AV721454.1  GI:10818606
KEYWORDS    EST.
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human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 658)  
Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X.,  
Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,  
S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R.,  
Chen,Z., Chen,Z. and Han,Z.  
Homo sapiens cdNA HTB clones  
Unpublished (2000)  
Contact: Zequang Han  
Chinese National Human Genome Center at Shanghai  
331 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
201203, P. R. China  
Tel: 86-21-50801919(ex.45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn  
This clone is available at CHGC in Shanghai.  
Location/Qualifiers  
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/db\_xref="taxon:9606"  
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/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 181 a 151 c 176 g 149 t 1 others

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Best Local Similarity 78.5%; Pred. No. 7.6e-67;  
Matches 339; Conservative 0; Mismatches 85; Indels 8; Gaps 3;

QY 1 GGAGATGGATAAACCGTGTGAGTGCCTCAAGTTGTGTGGGACCATGGAATGGGAGACTG 60  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 219 GGAGATGGACAAACCGTGTGGTGCCTCCAGGTGTGTGACCATGGAACGGGAGACCG 278  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 61 GAGGGATACATGATCCCACTACAGGCCCAAGTCTCCAGTATGAGCCATGAGCCAGTT 120  
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Db 279 GAGGGATCCATGGTATTCAACCGTGGCGCTGTTACCTCCAGTACGAGCCATGAGCCAGCG 338  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 121 GAATCTGAATGTGAAGATGGAATCAAGACCGACGAGAGTGCACACTGACGTCAACCCCTCAT 180  
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Db 339 GAATCTGAATGCAAGACAGAACAAAGGCGCGACCGGAGTCAATATGATCAACACCCCAT 398  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 181 AACATGGGGTTCAGATCAAGAAAACACACCAAGAGCTGAGAAACTGGTGTAGTGCCAGGG 240  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 399 AACATGGGGCAGATCAAGAAAACACACATGACGTGAGAAACTACTGGAGGCCAGGG 458  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 241 TCAGGCAAAACCCCTGACTCCATGTTTATGGCCATGCTAGCTGTAATATCTGTGCAGT 300  
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Db 459 TCAGGC---AACCCCTGACTCCATGTTCTTGGCCATGCTAGCTAGTGTCTGTGCGGT 515  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 301 ATGATTTTCTGTCGAAGCAAAAACATATGGGCATATTTTCCCTAACCCACGGTAGT 360  
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Db 516 ATGTTTCCCTCTGTAGAGGC---ACATATGGGCATATGTTCTCTAATCCACTTGTAGT 571  
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QY 361 GTGATCATCATCTGAAGCAGCATCTCTCTTGACATATATCATCATCAAGGAGCATCAGT 419  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 572 ACGACTGGTACTGTGAGCGACACTTTCTCTGAGATATCATATGATCATGAGCGTGGGC 631  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 420 ACCAGGACCTCT 431  
||||| ||||| |||||  
Db 632 ACCAGGATCCCT 643  
||||| ||||| |||||

RESULT 10  
AG183922  
LOCUS AG183922 743 bp DNA linear GSS 09-JAN-2002





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Query Match      21.8%; Score 217.8; DB 12; Length 524;
Best Local Similarity 78.4%; Pred. No. 1.2e-56;
Matches 261; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 1 GGAGATGATAAACCGTGTGAGTGCCTCCCAAGTTCGTGCGACCATGGAATGGGAGACTG 60
Db 187 GGAGATGGACAAACCGTGTGGGTGGTCCCGAGGTGTGTGACCATGGAACGGGAGACCG 246
QY 61 GAGGATACATGATCCCAAGTACAGGCCAGCTCCTCCAGTATGAGCCATGAGCCAGTT 120
Db 247 GAGGATCCATGATTCACACCGTGGCCCTGTACTCCAGTACAGCCATGAGCCAGCG 306
QY 121 GAATCTGAATGTGAAGTGAATGAAGACCGACGAGAGTCAACATGACGTCAACCCCTCAT 180
Db 307 GAATCTGAATGCAAGACAGACAGAAAGGCGCGACCGAGTCACAATGACATCCAAACCCCAT 366
QY 181 ACATGGGGTGCAGTCAAGAAACACACACAGCAAGCTGAGAACTGGTGTAGTGCAGGG 240
Db 367 AACATGGGACAGATCAAGAAACACACACAGCAAGCTGAGAACTGGTGTAGTGCAGGG 426
QY 241 TCAGCAAAAACCCCTGACTCCTCATTTATGGCCATGTGTGTAATATCTGTGTCAGT 300
Db 427 TCAGCAAAAACCCCTGACTCCTCATTTATGGCCATGTGTGTAATATCTGTGTCAGT 486
QY 301 ATGATTTTCTGTGAGAGCAAGCAAAACATATTG 333
Db 487 TATAGGATCGGGTGAACCAACCAACCGCAATTG 519

RESULT 15
BI115904
LOCUS      576 bp      mRNA      linear      EST 26-JUN-2001
DEFINITION 602866576F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:5015106 5',
            mRNA sequence.
ACCESSION  BI115904
VERSION    BI115904.1 GI:14566805
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE  1 (bases 1 to 576)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-re@mail.nih.gov
            Tissue Procurement: DCTD/DTP
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM1823 row: h column: 19
            High quality sequence stop: 576.
            Location/Qualifiers
                1..576
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:5015106"
                /clone_lib="NIH_MGC_7"
                /tissue_type="small cell carcinoma"
                /cell_line="MGC3"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
            EcoRI; cDNA made by oligo-dT priming. Directionally
            cloned into EcoRI/XhoI sites using the following 5'
            adaptor: GGCACGAG(G). Size-selected >500bp for average
            insert size 1.8kb. Library constructed by Ling Hong in
            the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies)."
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BASE COUNT 169 a 143 c 171 g 93 t

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ORIGIN
Query Match      21.8%; Score 217.8; DB 13; Length 576;
Best Local Similarity 78.4%; Pred. No. 1.3e-56;
Matches 261; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 1 GGAGATGATAAACCGTGTGAGTGCCTCCCAAGTTCGTGCGACCATGGAATGGGAGACTG 60
Db 189 GGAGATGGACAAACCGTGTGGGTGGTCCCGAGGTGTGTGACCATGGAACGGGAGACCG 248
QY 61 GAGGATACATGATCCCAAGTACAGGCCAGCTCCTCCAGTATGAGCCATGAGCCAGTT 120
Db 249 GAGGATCCATGATTCACACCGTGGCCCTGTACTCCAGTACAGCCATGAGCCAGCG 308
QY 121 GAATCTGAATGTGAAGTGAATGAAGACCGACGAGAGTCAACATGACGTCAACCCCTCAT 180
Db 309 GAATCTGAATGCAAGACAGACAGAAAGGCGCGACCGAGTCACAATGACATCCAAACCCCAT 368
QY 181 AACATGGGGTGCAGTCAAGAAACACACACAGCAAGCTGAGAACTGGTGTAGTGCAGGG 240
Db 369 AACATGGGGACAGATCAAGAAACACACACAGCAAGCTGAGAACTGAGAACTGAGCGCAGGG 428
QY 241 TCAGCAAAAACCCCTGACTCCTCATTTATGGCCATGTGTGTAATATCTGTGTCAGT 300
Db 429 TCAGCAAAAACCCCTGACTCCTCATTTATGGCCATGTGTGTAATATCTGTGTCAGT 488
QY 301 ATGATTTTCTGTGAGAGCAAGCAAAACATATTG 333
Db 489 TATAGGATCGGGTGAACCAACCAACCGCAATTG 521
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Search completed: December 24, 2002, 21:54:09  
Job time : 1116.8 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2002, 16:29:47 ; Search time 1108.8 seconds  
(without alignments)  
14620.861 Million cell updates/sec

Title: US-09-708-724A-3\_COPY\_99000\_100000  
Perfect score: 1001  
Sequence: 1 tggcgcgcgcgtagtcoc.....tttttccaccatcaactaa 1001

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_Other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	303.2	30.3	648	12 BE887242	BE887242 601508554
2	283.2	28.3	763	13 BI551044	BI551044 603195787
3	212.6	21.2	559	12 BG722262	BG722262 602693433
4	206	20.6	526	12 BF433607	BF433607 7q59g03.x
5	206	20.6	662	12 BE948806	BE948806 UI-M-BH3-
6	202	20.2	1143	11 AK006906	AK006906 Mus muscu

c	7	195.4	19.5	517	10	AW293335
	8	192	19.2	470	9	AI982914
	9	178	17.8	934	14	BM800032
	10	165.6	16.5	845	13	BI561035
	11	163.8	16.4	372	14	U46290
	12	156.6	15.6	757	13	BI086746
c	13	136	13.6	458	10	BE670624
	14	132.2	13.2	678	13	BI462516
	15	118.8	11.9	337	14	T07679
	16	118.6	11.8	487	9	AA991438
c	17	117.4	11.7	636	17	AG066329
	18	116.6	11.6	600	12	BF678990
c	19	116.4	11.6	480	17	AQ122880
c	20	116.2	11.6	537	17	AQ390912
c	21	115.6	11.5	693	17	AQ315247
	22	114.4	11.4	206	13	BM456815
	23	114.4	11.4	641	12	BF674369
c	24	113.8	11.4	598	9	AL134441
c	25	113.4	11.3	490	10	AW265073
c	26	113.2	11.3	651	17	B66038
c	27	113.2	11.3	2169	11	AF305815
c	28	113	11.3	737	9	AL602864
c	29	112.8	11.3	435	17	AQ132070
c	30	112.8	11.3	571	17	B95510
c	31	112.8	11.3	651	17	AG041999
c	32	112.6	11.2	301	9	AI311276
c	33	112.4	11.2	657	17	B02497
c	34	112.2	11.2	541	17	AQ456714
c	35	112.2	11.2	600	17	AQ393075
c	36	112.2	11.2	606	17	AQ345963
c	37	112.2	11.2	2580	11	BC024736
c	38	112	11.2	570	9	AL703987
	39	112	11.2	677	12	BG612299
c	40	111.8	11.2	460	17	AQ706891
c	41	111.8	11.2	673	17	AQ274719
c	42	111.4	11.1	515	9	AA665160
c	43	111.2	11.1	358	17	B72389
c	44	111.2	11.1	535	17	AQ391712
c	45	111.2	11.1	628	17	AG182392

## ALIGNMENTS

RESULT 1  
BE887242  
LOCUS BE887242 601508554F1 NIH\_MGC\_71 Homo sapiens cDNA clone IMAGE:3910044 5',  
DEFINITION mRNA sequence.  
ACCESSION BE887242  
VERSION BE887242.1 GI:10342334  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 648)  
AUTHORS NIH-MGC <http://mgc.mci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Cloned through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM9724 row: 1 column: 13  
High quality sequence stop: 588.  
Location/Qualifiers 1. 648

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/db_xref="taxon:9606"
/clone="IMAGE:3910044"
/clone_lib="NIH_MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.1 kb."
BASE COUNT      189 a 141 c 138 g 180 t
ORIGIN

Query Match      30.3%; Score 303.2; DB 12; Length 648;
Best Local Similarity 79.5%; Pred. No. 5.2e-49;
Matches 420; Conservative 0; Mismatches 78; Indels 30; Gaps 4;

QY 502 AGGGACTGAGCGGGGATCATCTCCAGGAAGGGGCTGAGTAGGAAGTGCAGCGCG--- 558
|||||
Db 1 AGGGACTGAGCGGGGAGGACCTCCCGGGGACCCAGCGAAGGAGGAGCGCGCGCGCGC 60
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QY 559 -----CACATCCTCTCTTTACCGGGGATGTGCAGGATTACCGTGAATCATGACATC 610
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Db 61 CCCAGCATCAGCTCTCTATTTCCCTGGGGATGTGCAGAAATACCATGAATATGACTC 120
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QY 611 GTATCTCTCGGAATACCAATGGGAAATTTGGAGTCTAGAAATATTTGCTCCATTTAG 670
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Db 121 GTCATCTGAGAAATATCAATGGGAAACTGGAGTCTAGAAATTTGCTACCATTTAG 180
|||||
QY 671 CCCACGGTTCCCACTAGTGTATTTGGGTGATGAAGTGTCCGGAA-----C 719
|||||
Db 181 CCCACGGTTCCCACTAGTGTATTTGGGTGATCAAAATTTCCCGAATGCAATTTGCACA 240
|||||
QY 720 AAATGCGCTGCCATGATAGTTTCTGAAAGTAACATGTTTGGTTTCCAGAACACAATA 779
|||||
Db 241 AATTACGCTGCTATGACAAATTTGGAAGTAACATGTTTGGTCCCGCCAGAACAAATA 300
|||||
QY 780 CAGACTCTGGAGCTTTAAGCACCTTTATATATTAATAGTTAA-----TGCTTTTAAGT 833
|||||
Db 301 CTGACTTTGGAGCTTTAAGCACCTTTATATGTTTATACGTTAATGCTTTTAATTAAGT 360
|||||
QY 834 CAGAGTAGTTTATCAAGGAATAATTTGAATGATTTGGAATGAAGCACTCCAGCATCTAAT 893
|||||
Db 361 CAGAATAGTTTATCAAGGAATAATTTGAATGATTTGGAATGAAGCACTCCATAGCATCTAAC 420
|||||
QY 894 TGTAGATGTCCTTCTCTATACATACAAATCATTTCCAGGAAGGAAAGATAGGACCT 953
|||||
Db 421 TGTAGA--TCCAGCTCTCTCATACTACGAATGTTGCCAGGAAGAACAGTCAGGACCT 478
|||||
QY 954 TTGAAAAATCTGATGATCGGCGATGTGTTTTATCCACCATCACTAA 1001
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Db 479 GTGACAACTCTGATGAGTGGCATGAGTTTATCCACCATCACTAA 526
|||||

RESULT 2
BI551044
LOCUS
DEFINITION      603195787F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5275580 5',
mRNA sequence.
ACCESSION      BI551044
VERSION        BI551044.1 GI:15438356
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 763)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
```

```
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11695 row: m column: 21
High quality sequence stop: 692.

FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5275580"
/clone_lib="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
/Note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.5 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      236 a 143 c 148 g 236 t
ORIGIN

Query Match      28.3%; Score 283.2; DB 13; Length 763;
Best Local Similarity 83.6%; Pred. No. 3.6e-45;
Matches 363; Conservative 0; Mismatches 53; Indels 18; Gaps 3;

QY 584 TCCAGGATTTACCGTGAATCATGACTCGTCATCTCGCAATTTACCAATGGGAAATTTGA 643
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Db 37 TTCAGAAATTTACCATGAATATGACTCGTCATCTCGAGAAATTTCAATGSGGAAACTGA 96
|||||
QY 644 GTCTAGAAATTTATGCTCCATTTTAGCCCCACCGGTTCCCGAGTACGCTGATTTGGGGTGA 703
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Db 97 GTCTAGAAATTTATGCTACCATTTTAGCCCCACCGGTTCCCGAATTTATATTGGGTGA 156
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QY 704 TGAAGTGTCTCCGGAA-----CAATGCGTGGCATGATAGTTTCTGCAAAAGTA 752
|||||
Db 157 TAAATGTTCCCGAATGCAATTTGCACAAATTCAGCTGCTATGACAAATTTGTGCAAAAGTA 216
|||||
QY 753 ACATGTTTGGTTTCCAGAACACATACAGACTCTGGAGCTTTTAAAGCACCTTTATATGCT 812
|||||
Db 217 ACATGTTTGGTCCCGCCAGACACATAGTACTTTGGAGCTTTTAAAGCACCTTTATATGCT 276
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QY 813 TATTAGTTAATGCT-----TTTAAAGTCAGAGTAGTTTATCAAGGAAATTTGAATGATT 867
|||||
Db 277 TATTAGTTAATGCTTTTAAATTTAAGTCAGATAGTTTATCAAGGAAATTTGAATGATT 336
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QY 868 GGAATAAGGACTCCAGCATCTAATTTAGATGTCCTCAATTTCTTCATCACTACAATCA 927
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Db 337 GGAATAAGGACTCCATAGCATCTAATCTAGTA--TCCAGTCTCTTCATCACTACGAATGG 394
|||||
QY 928 TTTTCAGGAAGGAAAGATAGGACCTTTCAAAATCTGATGATCGGCCATGTGTTTTTA 987
|||||
Db 395 TTTCAGGAGGAGAAAGTAGTGAGGACCTGTGAAAAATCTGATGAGTCTGCCATGAGTTTTTA 454
|||||
QY 988 TCCACCATCACTAA 1001
|||||
Db 455 TCCACCATCACTAA 468

RESULT 3
BG722262
LOCUS
DEFINITION      602693433F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4825616 5',
mRNA sequence.
ACCESSION      BG722262
VERSION        BG722262.1 GI:14001449
KEYWORDS       EST.
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SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 559)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: Miklos Palkovits, M.D., Ph.D.
            Tissue Procurement: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L1AM10739 row: a column: 09
            High quality sequence stop: 559.

FEATURES    Location/Qualifiers
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                /lab_host="DH10B"
                /note="Organ: testis; Vector: pBluescriptR (modified
                pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
                size-selected for average insert size 2.2 kb and
                normalized to ROT 5. This is a primary library enriched
                for full-length clones and constructed using the
                Cap-trapper method (Carninci, in preparation). Library
                constructed by M. Brownstein (NIH/NHGRI, National
                Institutes of Health). Note: this is a NIH_MGC Library."
            93 a 200 c 173 g 93 t

BASE COUNT  93 a 200 c 173 g 93 t
ORIGIN

Query Match      21.2%; Score 212.6; DB 12; Length 559;
Best Local Similarity 75.7%; Pred. No. 1.8e-31;
Matches 308; Conservative 0; Mismatches 84; Indels 15; Gaps 3;

QY 284 GGTTTTGGCGCGCGTGGTGTCTCTGCTGCCAGAGTTTGGAACTGGAGATGCGCTC 343
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 153 GCTCCTGCGTGGCGCGTGGTGTCTCTGCTGCCAGAGTTTGGAACTGGAGATGCGCTC 212
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 344 TTCCTTCTCAGCAGACAGACCATG-AGCCTAGCGGAGCGGCCGCTTCGCGAAGCTCCCC 402
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 213 GTCCCTGCTCAGGCGAGAACCATGAAACCCGGCGGAGCGCGCGCGGCGGATGCTCCCT 272
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 403 CTCGCCAACGCGCGCTCCTCAGAGCGGT--CCGTGCGCGCGCTGCCGCGAGCTGACC 459
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 273 CTCGCCGAGTGGCGCGCCCTCAGTCTCAGCTTTCACGCGCTGCTGAGCGCCGATC 332
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QY 460 CGCAGCGCAGTGCAGAGTGTCTCTGTTGGCGGTGACAGGAGGAGGAGTGGAGCGGCGGA 519
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 333 CGCAGCGCAGCAAGAAATTGCTCTGTTGGCGGCGCGGCGGAGGAGTGGAGCGGCGAG 392
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 520 TCATCTCCAGGAAGCGGCTGAGTAGGAACGTGACGCCG-----CACATCCTCT 568
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 393 ACCTCCCGGGGACCCGAGGAGGAGCGCGAAGCGCGCGCCGCCCGCAGCATCACGCTCCT 452
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QY 569 CTTTACCGGGGATGTCAGGATACCGTGAATCATGACTCGTCACTTCCTCGAATACC 628
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 453 ATTTCCCTGGGGATGTGCAGAAATTTACCATGAATTTATGACTCGTCACTTCCTCGAATATC 512
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 629 AATGGGAAATTTGAGTCTAGAAATTTATGCTCCTCATTTTACGCCAC 675
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 513 AATGGGAAACTGGAGTCTAGAAATTTATGCTCCTCATTTTACGCCAC 559
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4
BE948806
LOCUS
DEFINITION UI-M-BH3-avj-h-01-0-UI.s1 NIH_BMAP_M_S4 Mus musculus cDNA clone
linear EST 03-OCT-2000
662 bp mRNA
NIH_BMAP_M_S4
```







Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 517)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html  
 Seq primer: M13 Forward  
 POLYA=Yes.

#### FEATURES

Location/Qualifiers

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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2726801"  
 /clone\_lib="NCI-CGAP\_Sub4"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; The NCI-CGAP Sub4 library is a subtracted library derived from the NCI-CGAP\_Sub2 library which is a subtracted library derived from the NCI-CGAP\_Sub1 library, which is a subtracted library derived from BI. BI constitutes a mixture of 21 normalized or subtracted NCI-CGAP libraries: NCI-CGAP\_Co4, NCI-CGAP\_Pr22, NCI-CGAP\_Pr28, NCI-CGAP\_Co10, NCI-CGAP\_Co16, NCI-CGAP\_Kid5, NCI-CGAP\_Kid12, NCI-CGAP\_Kid3, NCI-CGAP\_Kid11, NCI-CGAP\_Lym2, NCI-CGAP\_Br2, NCI-CGAP\_Co8, NCI-CGAP\_CLL1, NCI-CGAP\_Le12, NCI-CGAP\_Brn23, NCI-CGAP\_Lu5, NCI-CGAP\_Lu24, NCI-CGAP\_Lu19, NCI-CGAP\_GC4, NCI-CGAP\_GC6, NCI-CGAP\_Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below:  
 NCI-CGAP\_Kid3 pool 1 : LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE Clonoids 1323376-1323911, 1456008-1456775, 1500552-1502855) NCI-CGAP\_Kid5 pool 1 : LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonoids 1323912-1325831, 1471368-1472903, 1492104-1493255) NCI-CGAP\_Lu5 pool 1 : LLAM 3575-3582, 3851-3854 (IMAGE Clonoids 1414920-1417991, 1520904-1522439) NCI-CGAP\_GC4 pool 1 : LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clonoids 1257096-1258631, 1469064-1470983, 1475592-1476743) NCI-CGAP\_Pr22 pool 1 : LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonoids 985608-986759, 1101192-1101959, 1217928-1220615) NCI-CGAP\_Co10 pool 1 : LLAM 2644-2653, 2871-2872 (IMAGE Clonoids 1057416-1061255, 1144584-1145351) Subtraction was performed as previously described [Bonaldi, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.]  
 TAG\_LIB=NCI-CGAP\_Lu5  
 TAG\_TISSUE=lung  
 TAG\_SEQ=CAAC\*

BASE COUNT 159 a 75 g 188 t

ORIGIN

Query Match 19.5%; Score 195.4; DB 10; Length 517;  
 Best Local Similarity 99.5%; Pred. No. 4e-28;  
 Matches 196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 805 TTATATGTTATTAGTCTTTTAACTCAGAGTAGTTTATCAAGGAAATTTGAATG 864  
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 Db 517 TTATATGTTATTAGTCTTTTAACTCAGAGTAGTTTATCAAGGAAATTTGAATG 458

QY 865 ATTGGAATAGGACTCCACAGCATCTAATTGTAGATGTCCAATTCTTCTCATACTACAAA 924  
 |||||  
 Db 457 ATTGGAATAGGACTCCACAGCATCTAATTGTAGATGTCCAATTCTTCTCATACTACAAA 398  
 |||||  
 QY 925 TCATTTCCAGGAAGAAAGATAGGACCTTTGAAAAATCTGATGATCGGCGCATGTCTTT 984  
 |||||  
 Db 397 TCATTTCCAGGAAGAAAGATAGGACCTTTGAAAAATCTGATGATCGGCGCATGTCTTT 338  
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 QY 985 TTATCCACCACATCACTAA 1001  
 |||||  
 Db 337 TTATCCACCACATCACTAA 321  
 |||||  
 RESULT 8  
 AI982914  
 LOCUS w229f09.x1 NCI\_CGAP\_Brn53 Homo sapiens cDNA clone IMAGE:2559497 3', mRNA linear EST 09-MAR-2000  
 DEFINITION mRNA sequence.  
 ACCESSION AI982914  
 VERSION AI982914.1 GI:5810133  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 470)  
 NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGP), Tumor Gene Index  
 Unpublished (1998)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html  
 Insert length: 3011 Std Error: 0.00  
 Seq primer: -400P from Glibco  
 High quality sequence stop: 408.  
 FEATURES Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2559497"  
 /clone\_lib="NCI\_CGAP\_Brn53"  
 /tissue\_type="three pooled meningiomas"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: pCMV-SPORT6; Site.1: SalI; Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies."  
 BASE COUNT 79 a 167 c 142 g 80 t 2 others  
 ORIGIN  
 Query Match 19.2%; Score 192; DB 9; Length 470;  
 Best Local Similarity 74.7%; Pred. No. 1.9e-27;  
 Matches 284; Conservative 0; Mismatches 82; Indels 14; Gaps 3;  
 QY 284 GGTTTTGGGTGCGCGGTGTTGCTGCTGCTGCCACAGCTTGGAACTGGAGATGCCTC 343  
 |||||  
 Db 91 GCTCCTGGGTGCGCGGTGTTGCTGCTGCTGCCAGCTCGGAATCGGAACGGCTC 150  
 |||||  
 QY 344 TTCTTCTCTCAGGACAGAACCATG-AGCCTAGCGGAGCGCCGGTTGCGGAAGTCCCC 402  
 |||||  
 Db 151 GTCTGTCTCTCAGGACAGAACCATGAACCCGGCGGAGCGCGCGCATGTCTCCT 210  
 |||||  
 QY 403 CTCGCCAACGGCGCTCTCTCAGAGCGGTCC--GTGCCCGCCCTGCCGGAGCTGACCC 460  
 |||||  
 Db 211 CTCGCCAGAGTGGCGCGGCGCTCAGTGCCTTCCACCGTGCCTGGAGCGGATCC 270

```
Qy 461 GCAGCGCAGTCGAGAGTTGCTCTCTGTTGGCGGTGACCGAGGAGGAGGACTGGAGCGCGGAT 520
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 271 GCAGCGCAGCACGAATGCTCTGTTGGCGCGCGCGGAGGAGGACTGGAGCGCGAGA 330
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 521 CATCTCCAGGAGCGGGCTGAGTAGGAAGTGCAGCCG-----CACATCCTCTC 569
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 331 CTCTCCCGGNGACCCAGGAGGAGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCTCTA 390
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 570 TTTACCCGGGATGTCAGGATTACCGTGAATCATGACTCGTCATCTCGCGAAATTACCA 629
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 391 TTTCCCTGGGATGTCAGAATTACCATGAATTAAGTCTGCTCACTCTGAGAAATTATCA 450
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 630 ATGGGAAAATTGGAGCTAG 649
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 451 ATGGGAAAATGGAGCTAG 470
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

RESULT 9
BM800032
LOCUS
DEFINITION BM800032 934 bp mRNA linear EST 05-MAR-2002
5' mRNA sequence.
ACCESSION BM800032
VERSION BM800032.1 GI:19116855
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapb-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12212 row: a column: 11
High quality sequence stop: 531.
FEATURES
Location/Qualifiers
1..934
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5531026"
/clone_lib="NIH_MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."
BASE COUNT 303 a 139 c 213 g 279 t
ORIGIN
Query Match 17.8%; Score 178; DB 14; Length 934;
Best Local Similarity 87.3%; Pred. No. 7.6e-25;
Matches 220; Conservative 0; Mismatches 25; Indels 7; Gaps 2;

Qy 755 ATGTTTGTTCCAGACAAATACAGACTCTGGAGCTTTTAAGCACCCTTATATGTTA 814
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1 ATGTTTGTTGCCAGACAAATACTACTGCTTGGAGCTTTTAAGCACCCTTATATGTTA 60
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 815 TTAGTTAATGCT-----TTTAAGTCAGAGTAGTTTATCAAAAGGAAAATTTGAATGATGG 869
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 61 TTAGTTAATGCTTTTAATTTAAGTCAGAGTAGTTTATCAAAAGGAAAATTTGAATGTTGG 120
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 870 AATAAGGACTCCACAGCATCTAAATTGTAGATGTCCAAATCTTCTCATACTACAAATCAT 929
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
```

```
Db 121 AATAAGGACTCCATAGCATCTAACTAGTGTAGA--TCAGATCCTTCTCATACTACGAATGTT 178
Qy 930 TCCAGGAAGGAAAGATAGGACCTTTGAAAAATCTGATGATCGCGCATGTCTTTTATC 989
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 179 GCCAGGAGAAAAGTGGAGACCTGTGAAAAATCTGATGATGAGTCTGCCATGAGTTTATC 238
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 990 CACCATCACTAA 1001
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 239 CACCATCACTAA 250
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

RESULT 10
BI561035
LOCUS
DEFINITION BI561035 845 bp mRNA linear EST 05-SEP-2001
603254237F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5296617 5',
mRNA sequence.
ACCESSION BI561035
VERSION BI561035.1 GI:15448349
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapb-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11750 row: j column: 10
High quality sequence stop: 559.
FEATURES
Location/Qualifiers
1..845
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5296617"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTNN-3',
size-selected for average insert size 2.2 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 206 a 253 c 239 g 147 t
ORIGIN
Query Match 16.5%; Score 165.6; DB 13; Length 845;
Best Local Similarity 74.8%; Pred. No. 2e-22;
Matches 305; Conservative 0; Mismatches 84; Indels 19; Gaps 7;

Qy 284 GGTTTTGGCGTGGCGGTGTTGCTCTGCTGCCAGAGCCCGGTTCGCGAAGTCCCTC 343
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 178 GCTCCTGGGTGGCGCGGTGCTGCTCTGCTGCCAGAGTCCGGAATCGGAAGCGCTC 237
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 344 TTCCTTCTCTCAGGACAGAACCATG-AGCCTAGCGGAGCGCGCGGTTCGCGAAGTCCCTC 402
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 238 GTCCTGCTCTCAGGCCAGAACCATGAAACCGGCGGAGCGCGCGATGCTCCCT 297
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 403 CTCGCGCAACGGGCGCTCTCTCAGAGCGGTCC--GTGCGCGCGCTTCGCGGAGTGAACC 460
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 298 CTCGCGCGAGGTGGCGCGCGCTCAGTGCCTTCAGCTTTCCACCGTGCCTGGAGCGCATCC 357
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
```

Qy	521	CATCTCCAGGAAGCGGCTGAGTAGGAACATGCACCGCG-----CACATCCTCTC	569
Db	241	CCTCCCGGGACCCAGGAAGGAGGCGCGNAGNCGCCGCCCGCCAGNATCACGTCCTCTA	300
Qy	570	TTTACCCTGGGATGTGAGGATTTACCCTGGAATCATCATCGTCATCCTCGGAATTACCA	629
Db	301	TTTCTNCCTGGGATGTGAGAAATTTACCATGAATTTATGACTCGNCTATCCTGAGAATTATCA	360
Qy	630	ATGGGAAAATTG 641	
Db	361	ATGGGAAAACATG 372	
RESULT 12			
BI086746			
LOCUS	602850217F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4991524 5',	757 bp mRNA linear EST 20-JUN-2001	
DEFINITION	mRNA sequence.		
ACCESSION	BI086746		
VERSION	BI086746.1 GI:14505076		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 757)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-femail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Incyte Genomics, Inc. DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM1009 row: b column: 05 High quality sequence start: 7 High quality sequence stop: 633. Location/Qualifiers 1..757 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4991524" /clone_lib="NIH_MGC_10" /cell_line="MGC36" /lab_host="DH10B" /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.5 kb. Library prepared by Life Technologies."		
BASE COUNT	239 a 134 c 166 g 218 t		
ORIGIN			
Query Match	15.6%; Score 156.6; DB 13; Length 757;		
Best Local Similarity	84.9%; Pred. No. 1.1e-20;		
Matches 213; Conservative	0; Mismatches 29; Indels 9; Gaps 3;		
Qy	757	GTTTGGTTTCCAGAACACATACAGACTCTGGAGCTTTTAAGCACCTTTATATGTTATT	816
Db	1	GTTAGTGCCCGAGACAAATACTGACT-TGGAGCTTTGAAGCACCTTTATATGTTATT	59
Qy	817	AGTTAATGCTTTTAAAGTCA-----GAGTAGTTTATCAAGGAAAATTTGAATGATTGGA	870
Db	60	AGTTAATGCTTTGAATTTAAGTCAGAAGTAGTTTATCAAGAAAAAGTTTGAATGTTGGA	119
Qy	871	ATAGGACTCCACAGCATCTAATTGTAGATGCCAATTTCTCTCATACTACAAATCATTT	930
Db	120	ATAGGACTCCATAGCATCTAACTGTAGA--TCCAGTCTCTTCTCATACTAGCAATGGTTG	177

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Qy 931 CCAGGAAGAAAGATAGGACCTTTGAAAAATCTCATGATCGGCCATGTGTTTTATCC 990
||||| ||| ||||| ||||| ||||| ||||| ||| ||||| ||||| |||||
Db 178 CCAGGAGAAAAAGTGAGGACCTGTGAAAAATCTCATGATCGGCCATGTGTTTTATCC 237
||||| ||| ||||| ||||| ||||| ||||| ||| ||||| ||||| |||||
Qy 991 ACCATCACTAA 1001
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 238 ACCATCACTAA 248
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
BE570624/c
LOCUS BE570624 458 bp mRNA linear EST 08-SEP-2000
DEFINITION 7e37d08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284655 3',
mRNA sequence.
ACCESSION BE570624
VERSION BE570624.1 GI:10031165
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 458)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco.
Location/Qualifiers
1. 458
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3284655"
/clone_lib="NCI_CGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="DH10B"
/notes="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI_CGAP_Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (cloneIDs
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 137 a 84 c 70 g 167 t
ORIGIN
Query Match 13.6%; Score 136; DB 10; Length 458;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 866 TTGGAATAAGGACTCCAGCATCTAATTGTAGATGTCCAATCTTCTCATACTACAAT 925
||||| ||| ||||| ||||| ||||| ||||| ||| ||||| ||||| |||||
Db 458 TTGGAATAAGGACTCCAGCATCTAATTGTAGATGTCCAATCTTCTCATACTACAAT 399
||||| ||| ||||| ||||| ||||| ||||| ||| ||||| ||||| |||||
Qy 926 CATTTCCAGGAAGAAAGATAGGACCTTTGAAAAATCTGATGATCGGCCATGTGTTTT 985
||||| ||| ||||| ||||| ||||| ||||| ||| ||||| ||||| |||||
Db 398 CATTTCCAGGAAGAAAGATAGGACCTTTGAAAAATCTGATGATCGGCCATGTGTTTT 339
||||| ||| ||||| ||||| ||||| ||||| ||| ||||| ||||| |||||
Qy 986 TATCCACCATCACTAA 1001
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 338 TATCCACCATCACTAA 323
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
RESULT 14
LOCUS BI462516
DEFINITION 603209421F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5271245 5',
mRNA sequence.
ACCESSION BI462516
VERSION BI462516.1 GI:15253172
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 678)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11684 row: i column: 06
High quality sequence stop: 645.
Location/Qualifiers
1. 678
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5271245"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/notes="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgaag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.2 kb and
normalized to R0r 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 126 a 219 c 206 g 127 t
ORIGIN
Query Match 13.2%; Score 132.2; DB 13; Length 678;
Best Local Similarity 67.6%; Pred. No. 6.2e-16;
Matches 298; Conservative 0; Mismatches 118; Indels 25; Gaps 7;

Qy 284 GGTGTTTGGGTGCGCGGTGCTCTTCTGCTGCCACAGGTTGGAATGGAGATGCCTC 343
||||| ||| ||||| ||||| ||||| ||||| ||| ||||| ||||| |||||
Db 158 GCTCTCTGCGGTGCGCGGTGCTCTGCTGCCAGCTCGGAATCGGAACGCCTC 217
||||| ||| ||||| ||||| ||||| ||||| ||| ||||| ||||| |||||
Qy 344 TTCCTTCTCTCAGACAGAACCATG-AGCTAGCGCGAGCCGCTTCGCGAGCTCCCC 402
||||| ||| ||||| ||||| ||||| ||||| ||| ||||| ||||| |||||
Db 218 GTCTGTGCTCTCAGGCCAGAACCATGAACCGGGCGGAGCGGATGCTCCCT 277
||||| ||| ||||| ||||| ||||| ||||| ||| ||||| ||||| |||||
Qy 403 CTCGCCCAACGGCGCCCTCTCTCAGAGCGTCCGTGC-----CGCCCTCGCGGAGCT 455
||||| ||| ||||| ||||| ||||| ||||| ||| ||||| ||||| |||||
Db 278 CTCGCCCGAGGTGCTGCGGGGATCAGTGCCTTCAGCTTTTCCACCTGCTGGAGCC 337
||||| ||| ||||| ||||| ||||| ||||| ||| ||||| ||||| |||||
Qy 456 GACCCGCGACGCGAGTGCAGAGTTGCTCTGTGGCGGTGACACGAGGAGGACTGGAGCGG 515
||||| ||| ||||| ||||| ||||| ||||| ||| ||||| ||||| |||||
Db 338 GATCCGCGACGACGACGAATGCTCTGTGTGGCGGCGCGGAGGAGGACTGGAGCGG 397
||||| ||| ||||| ||||| ||||| ||||| ||| ||||| ||||| |||||
Qy 516 C-GGATCATCTCCAGGAGCGGCTGAGTAGGAATCGAGCC-----GCCACATC 564
||||| ||| ||||| ||||| ||||| ||||| ||| ||||| ||||| |||||
Db 398 CAGGACCTCCCGGGGACCCAGTCAAGAGGAGCGCGAGACCGCGGCAGATTCACGTC 457
||||| ||| ||||| ||||| ||||| ||||| ||| ||||| ||||| |||||
Qy 565 CTCCTCTTTACCCGGGATGTGCAGGA--TTACCGTGAATCATGACTCGTCATCCTCGGA 622
||||| ||| ||||| ||||| ||||| ||||| ||| ||||| ||||| |||||
```



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2002, 16:29:47 ; Search time 1108.8 Seconds  
(without alignments)  
14620.861 Million cell updates/sec

Title: US-09-708-724a-3\_COPY\_10000\_11000  
Perfect score: 1001  
Sequence: 1 caaaatttcagtttaggaaga.....gcagcacataatgatcatg 1001

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- EST:\*
- 1: em\_estba:\*
  - 2: em\_esthum:\*
  - 3: em\_estin:\*
  - 4: em\_estmu:\*
  - 5: em\_estov:\*
  - 6: em\_estpl:\*
  - 7: em\_estro:\*
  - 8: em\_hic:\*
  - 9: gb\_est1:\*
  - 10: gb\_est2:\*
  - 11: gb\_hic:\*
  - 12: gb\_est3:\*
  - 13: gb\_est4:\*
  - 14: gb\_est5:\*
  - 15: em\_estfun:\*
  - 16: em\_estom:\*
  - 17: gb\_gss:\*
  - 18: em\_gss\_hum:\*
  - 19: em\_gss\_inv:\*
  - 20: em\_gss\_pln:\*
  - 21: em\_gss\_vrt:\*
  - 22: em\_gss\_fun:\*
  - 23: em\_gss\_mam:\*
  - 24: em\_gss\_mus:\*
  - 25: em\_gss\_other:\*
  - 26: em\_gss\_pro:\*
  - 27: em\_gss\_rod:\*

Pred. | No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	354	35.4	637	9	AL705037 DKFZp686C
2	354	35.4	694	9	AL704947 DKFZp686L
3	206.4	20.6	949	14	BQ230091 AGENCOURT
4	188.8	18.9	391	17	AQ093103 HS_3020_B
5	119	11.9	371	9	AA417076 zul3b12.s
6	113.6	11.3	397	9	AA417055 zul3b12.r

c	7	89.2	8.9	432	17	B50982	B50982 CIT978SK-19
c	8	85.6	8.6	726	17	AG153358	AG153358 Pan trogl
c	9	84.6	8.5	296	14	T39269	T39269 Ya03b03.r2
c	10	83.4	8.3	495	17	AQ134321	AQ134321 HS_3051_B
c	11	83.4	8.3	518	17	AQ169197	AQ169197 HS_3175_B
c	12	83.2	8.3	689	17	AQ779816	AQ779816 HS_5572_B
c	13	82.8	8.3	689	17	AG183488	AG183488 Pan trogl
c	14	82.4	8.2	391	14	T05554	T05554 EST03443 Fe
c	15	82.4	8.2	550	17	AQ468873	AQ468873 HS_5140_B
c	16	82.2	8.2	670	10	AV731805	AV731805 AV731805
c	17	81.8	8.2	522	17	AQ547767	AQ547767 RPCI-11-3
c	18	81.2	8.1	661	17	AQ127758	AQ127758 Pan trogl
c	19	80	8.0	455	17	AQ698289	AQ698289 HS_5551_B
c	20	79.6	8.0	750	14	BM981428	BM981428 UI-CF-EN1
c	21	79.6	8.0	514	12	BF080764	BF080764 231769 MA
c	22	78.4	7.8	626	10	AQ118584	AQ118584 HS_3012_A
c	23	77.6	7.8	696	17	AQ031398	AQ031398 Pan trogl
c	24	77.2	7.7	614	17	AQ240524	AQ240524 CIT-HSP-2
c	25	77.2	7.7	395	9	AI263349	AI263349 qql3a08.x
c	26	77.2	7.7	524	17	AQ804711	AQ804711 HS_3094_A
c	27	76.4	7.6	490	17	AQ819320	AQ819320 HS_5295_A
c	28	76.4	7.6	448	17	B60070	B60070 CIT-HSP-387
c	29	75.8	7.6	330	17	B86003	B86003 RPCI-11-2L1
c	30	75.8	7.6	399	9	AI203367	AI203367 qr24h10.x
c	31	75.6	7.6	729	17	AG013623	AG013623 Homo sapi
c	32	75.4	7.5	665	17	AG171538	AG171538 Pan trogl
c	33	75.2	7.5	391	12	BE701171	BE701171 PM3-NN012
c	34	75.2	7.5	470	17	B98998	B98998 CIT-HSP-228
c	35	75.2	7.5	409	17	AQ712786	AQ712786 HS_5387_A
c	36	74.8	7.5	388	9	AA581747	AA581747 nn48a05.r
c	37	74.4	7.4	729	17	AG105429	AG105429 Pan trogl
c	38	74.2	7.4	744	17	AQ480400	AQ480400 RPCI-11-2
c	39	73.8	7.4	401	14	R96184	R96184 vt84g10.r1
c	40	73.8	7.4	471	14	BQ234610	BQ234610 hd47f06.g
c	41	73.8	7.4	530	17	AQ420934	AQ420934 RPCI-11-2
c	42	73.8	7.4	536	17	AQ415616	AQ415616 RPCI-11-2
c	43	73.8	7.4	540	17	AQ785791	AQ785791 HS_5547_A
c	44	73.8	7.4	574	14	BQ234796	BQ234796 hd50b02.g
c	45	73.8	7.4				

ALIGNMENTS

RESULT 1	AL705037	AL705037	637 bp	mrna	linear	EST 22-MAR-2002
LOCUS	DKFZp686C1134_r1	686 (synonym: hlcc3)	Homo sapiens	cdna	clone	
DEFINITION	DKFZp686C1134 5', mRNA sequence.					
ACCESSION	AL705037					
VERSION	AL705037.1	GI:19688392				
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	1 (bases 1 to 637)					
TITLE	Ottawaelder, B., Obermaier, B., Mewes, H.W., Mewes, H.W., Weil, B. and Wiemann, S.					
JOURNAL	EST (Ottawaelder, B., Obermaier, B., Mewes, H.W., Mewes, H.W., Weil, B. and Wiemann, S.)					
COMMENT	Unpublished (2001) Contact: Ottawaelder B MIPS Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix (Martinsried/Germany) within the CDNA sequencing consortium of the German Genome Project. No sl sequence available. This clone (DKFZp686C1134) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059					

Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES  
source

1. .637  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="DKFZp686C1134"  
/clone\_lib="686 (synonym: hlcc3)"  
/tissue\_type="human skeletal muscle"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="vector: priplEx2; Site\_1: SfiIA; Site\_2: SfiIB;  
cdna-collection"

BASE COUNT 191 a 116 c 133 g 196 t 1 others  
ORIGIN

Query Match 35.4%; Score 354; DB 9; Length 637;  
Best Local Similarity 99.7%; Pred. No. 7.2e-64;  
Matches 365; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 637 TCCTGGGTATAGTGTAGTGTGTAATCTGTGTTTACATACAGGATAACATAAAACAAAGG 696  
|||||  
Db 1 TCCTGGGTATAGTGTAGTGTGTAATCTGTGTTTACATACAGGATAACATAAAACAAAGG 60  
  
Qy 697 TAAACAATAAATAAAACAGACAGCAAACTCAACTAATAGTGTGGCATGTGTGACA 756  
|||||  
Db 61 TAAACAATAAATAAAACAGACAGCAAACTCAACTAATAGTGTGGCATGTGTGACA 120  
  
Qy 757 GTGAAGACAGGAGCTGCATATAAATGGAGTGGGAAC-TTTTGAGCTAAATCAATGTCC 815  
|||||  
Db 121 GTGAAGACAGGAGCTGCATATAAATGGAGTGGGAACTTTTGAGCTAAATCAATGTCC 180  
  
Qy 816 TGTGTGTTTCTGTTTCTACATCAGACTCTATAGTGGCAATTCAGGTTAGTGTGTTT 875  
|||||  
Db 181 TGTGTGTTTCTGTTTCTACATCAGACTCTATAGTGGCAATTCAGGTTAGTGTGTTT 240  
  
Qy 876 TTATCCTTGCCTGCTAGTAAGTCCAGAGAGATTTTCTAAACTGGTGAGGAACAGG 935  
|||||  
Db 241 TTATCCTTGCCTGCTAGTAAGTCCAGAGAGATTTTCTAAACTGGTGAGGAACAGG 300  
  
Qy 936 TAGAAGAGTGAAGTGAGACAAACTTCCTGCTCATTTGCCAAGTGGCAGCACAATAGT 995  
|||||  
Db 301 TAGAAGAGTGAAGTGAGACAAACTTCCTGCTCATTTGCCAAGTGGCAGCACAATAGT 360  
  
Qy 996 ATCATG 1001  
|||||  
Db 361 ATCATG 366

RESULT 2  
AL704947 694 bp mRNA linear EST 22-MAR-2002  
LOCUS DKFZp686L2233.r1.686 (synonym: hlcc3) Homo sapiens cdna clone  
DEFINITION DKFZp686L2233 5', mRNA sequence.  
ACCESSION AL704947  
VERSION AL704947.1 GI:19688302  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 694)  
Ottewaelder, B., Obermaier, B., Mewes, H.W., Weill, B. and  
Wiemann, S.

EST (Ottewaelder, B., Obermaier, B., Mewes, H.W., Weill, B. and Wiemann  
, S.)  
Unpublished (2001)  
Contact: Ottewaelder B  
MIPS

Am Klopferspitz 18a D-82152 Martinsried, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by MediGenomix (Martinsried/Germany) within the cdna

sequencing consortium of the German Genome Project. No sl sequence  
available.  
This clone (DKFZp686L2233) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES  
source

1. .694  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="DKFZp686L2233"  
/clone\_lib="686 (synonym: hlcc3)"  
/tissue\_type="human skeletal muscle"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="vector: pTriplEx2; Site\_1: SfiIA; Site\_2: SfiIB;  
cdna-collection"

BASE COUNT 205 a 131 c 140 g 216 t 2 others  
ORIGIN

Query Match 35.4%; Score 354; DB 9; Length 694;  
Best Local Similarity 99.7%; Pred. No. 7e-64;  
Matches 365; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 637 TCCTGGGTATAGTGTAGTGTGTAATCTGTGTTTACATACAGGATAACATAAAACAAAGG 696  
|||||  
Db 1 TCCTGGGTATAGTGTAGTGTGTAATCTGTGTTTACATACAGGATAACATAAAACAAAGG 60  
  
Qy 697 TAAACAATAAATAAAACAGACAGCAAACTCAACTAATAGTGTGGCATGTGTGACA 756  
|||||  
Db 61 TAAACAATAAATAAAACAGACAGCAAACTCAACTAATAGTGTGGCATGTGTGACA 120  
  
Qy 757 GTGAAGACAGGAGCTGCATATAAATGGAGTGGGAAC-TTTTGAGCTAAATCAATGTCC 815  
|||||  
Db 121 GTGAAGACAGGAGCTGCATATAAATGGAGTGGGAACTTTTTGAGCTAAATCAATGTCC 180  
  
Qy 816 TGTGTGTTTCTGTTTCTACATCAGACTCTATAGTGGCAATTCAGGTTAGTGTGTTT 875  
|||||  
Db 181 TGTGTGTTTCTGTTTCTACATCAGACTCTATAGTGGCAATTCAGGTTAGTGTGTTT 240  
  
Qy 876 TTATCCTTGCCTGCTAGTAAGTCCAGAGAGATTTTCTAAACTGGTGAGGAACAGG 935  
|||||  
Db 241 TTATCCTTGCCTGCTAGTAAGTCCAGAGAGATTTTCTAAACTGGTGAGGAACAGG 300  
  
Qy 936 TAGAAGAGTGAAGTGAGACAAACTTCCTGCCAATTTGCCAAGTGGCAGCACAATAGT 995  
|||||  
Db 301 TAGAAGAGTGAAGTGAGACAAACTTCCTGCCAATTTGCCAAGTGGCAGCACAATAGT 360  
  
Qy 996 ATCATG 1001  
|||||  
Db 361 ATCATG 366

RESULT 3  
BO230091 949 bp mRNA linear EST 02-MAY-2002  
LOCUS AGENCOURT\_7575432 NIH\_MGC\_72 Homo sapiens cdna clone IMAGE:6049217  
DEFINITION 5', mRNA sequence.  
ACCESSION BO230091  
VERSION BO230091.1 GI:20411491  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 949)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP  
cdna Library Preparation: Life Technologies, Inc.  
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)



DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LENL at:  
<http://image.llnl.gov>  
Plate: L1AM13299 row: h column: 18  
High quality sequence stop: 587.

## FEATURES

BASE COUNT	266 a	234 c	222 g	226 t	1 others
ORIGIN					
Query Match	20.6%;	Score 206.4;	DB 14;	Length 949;	
Best Local Similarity	59.1%;	Pred. No. 3.7e-33;			
Matches 307;	Conservative 0;	Mismatches 116;	Indels 21;	Gaps 1;	
QY	294	AAAGAGGAAATAAGGATACAAAATGTCACACAGAGAGAGAAATGGCCACATGAGGACACAAAT	353		
Db	338	AGAGAGGAGATAGGATACAAATGTGCACACAGAGAAATGACCACTGAGGACACAAAG	397		
QY	354	GAGAATGTGGCTACTTTACAAGCCTTAGGAGAGCGCTCCGAGAAACACACACCCCTACCCAC	413		
Db	398	GAGAAGGTGGCCACTTTACAACCCCTAGGAGAGAGCCCTGGGGGCAACACACCCCTGCCAC	457		
QY	414	ACCTTGATGTTGGA-----CCTCATCCTGTGTAGCAAGTCTCTCC	452		
Db	458	ACCTTGACCTGGACTTTCATCCNCAGATAAAGTCTCTCATCTCCAGATAAAGTCTCTTC	517		
QY	453	ACCTCTCTTCATCAGGTGGAGCGCTTTGATCTCAATATCTCCAAATGCTGGAGGTAC	512		
Db	518	ATCCTCTCTCATCATATGGAACCTTCTGACCCCTGAATACTCTCCAAATGCTGTATGTAC	577		
QY	513	AAAAGTGAAGACAGACAGACACTCAGGGTGAAGAAGTTTAAACAGAAATACACTTTCC	572		
Db	578	CAGGTGAAGGGACAGACAGACACTCAGGTGTAAGAAGTTTAAAGAAGTAACTATTTCCC	637		
QY	573	ATTGCTGTGTCCTATCCCTACACACACCTATTCCAGTCTTTATTGGTCTTTTGTGTTTT	632		
Db	638	ATTGCCCTGTCCCATCCCCAACACACACCTGTGCCAGCCCTTTATTGGTCTTTTGTGTA	697		
QY	633	CGTGTCTCTGGGTATAGTGTGTAGTTGTAATCTGTGTTTACATACAGATAACATAAACA	692		
Db	698	TTCCCTCTGTCTGGGATATAGGGGGAACCTTTATTTAATCCTGGGCTTTATGTGTATA	757		
QY	693	AAGTAAACAATAAATAAACA	716		
Db	758	GGGATAACCCCTACAAACCAAGA	781		

RESULT 4	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
1	AQ093103/c	HS-3020_B1_A04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3020 Col-7 Row-B, DNA sequence.	AQ093103	1	GI:34564550	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Kellar, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D., and

[illegible]

RESULT 5	AA417076/c	AA417076	371 bp	linear	EST 09-NOV-1997
LOCUS		313b12.s1	Soares_testis_NHT	Homo sapiens	cdna clone IMAGE:731711
DEFINITION		3', mRNA sequence.			
ACCESSION		AA417076			
VERSION		AA417076			
KEYWORDS		AA417076.1	GI:2077158		
SOURCE		EST.			
ORGANISM		human.			
		Homo sapiens			
		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			







## ORIGIN

Query Match 8.3%; Score 83.4; DB 17; Length 518;  
 Best Local Similarity 67.9%; Pred. No. 1.8e-07;  
 Matches 131; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 240 TTTAAATGAGGACCTTAGGGTGGTCTTAATCCCAATCTAAGTGATGTCTCCATGA-AAGA 298  
 Db 173 TTTAAAGTGAGTTTATTTGAGTGGGCCCTTAATCCCAAAATGACTGATGTCAATGAAGATGA 232  
 QY 299 GGAATATAGGATACAAATGTGCACACAGAGAGAAATGCCACATGACAGACACAATGAGAA 358  
 Db 233 GGAATTTAGGACACACACACAGTGTACAGAGGAAGACCCAGTGAAGACCAAGGGGAT 292  
 QY 359 TGTGGCTACTTACAAAGCTTAGGAGAGAGGCTCGAGAGAAACACACCTTACCCACACTT 418  
 Db 293 GTGGCCATGTACAAAGCTTAGGACAGAGGCTTCGGGAGGAGCAACCCAGCCAAACACTT 352  
 QY 419 GATGTTGGACTTC 431  
 Db 353 GATTCAGACTTC 365

## RESULT 12

AQ779816  
 LOCUS HS.5572.B2.F11.SP6.RPCI-11 Human Male BAC Library Homo sapiens  
 DEFINITION genomic clone Plate=1148 Col=22 Row=L, DNA sequence.

ACCESSION AQ779816  
 VERSION AQ779816.1 GI:5682776  
 KEYWORDS GSS.

## SOURCE

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
 Hood,L.

## TITLE

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

99380589

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC  
 library availability, please contact Pieter de Jong  
 (pieterdejong.med.buffalo.edu). Clones may be purchased from  
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering\_bac.htm)  
 or from Research Genetics (info@resgen.com). BAC end Web Server:  
 http://www.htsc.washington.edu

Plate: 1148 row: L column: 22

Seq primer: SP6

Class: BAC ends

High quality sequence stop: 689.

## FEATURES

## source

Location/Qualifiers  
 1..689  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="Plate=1148 Col=22 Row=L"  
 /clone\_lib="RPCI-11 Human Male BAC Library"  
 /sex="male"

/notes="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;  
 Male blood DNA was isolated from one randomly chosen donor  
 and partially digested with a combination of EcoRI and  
 EcoRI Methylase. Size selected DNA was cloned into the  
 pBACe3.6 vector at EcoRI sites"

## BASE COUNT

193 a 155 c 179 g 161 t 1 others

## ORIGIN

Query Match 8.3%; Score 83.2; DB 17; Length 689;  
 Best Local Similarity 71.9%; Pred. No. 1.9e-07;  
 Matches 138; Conservative 0; Mismatches 48; Indels 6; Gaps 2;

QY 240 TTTAAATGAGGACCTTAGGGTGGTCTTAATCCCAATCTAAGTGATGTCTCCATGAAGAAG 299  
 Db 414 TTTAAATGAAGTCCTTAGGTTGGCCCTTAATCCAATGTGACTGGTGT--CCTTTTAAAGA 471  
 QY 300 GAAATATAGGATACAAATGTGCACACAGAGAGAAATGGCCACATGAGGACACACAATGAGAA 359  
 Db 472 GAGATTAGGACACACAGATGCACAGAGAGAGA----CCATGTGAAGACGCAAGGAAAAG 527  
 QY 360 GTGGCTACTTACAAAGCTTAGGAGAGAGGCTCCGAGAGAAACACACCTTACCCACACTTG 419  
 Db 528 ACAGCCATCTACAAGCCAAAGAGAGAGGCGCTCAGAAGAACCAACCCCTGCTGACACCTTG 587  
 QY 420 ATGTTGGACTTC 431  
 Db 588 ATCTTGAACCTC 599

## RESULT 13

AG183488/c  
 LOCUS Pan troglodytes DNA, clone: RP43-056P19.TJ, genomic survey  
 DEFINITION sequence.

ACCESSION AG183488  
 VERSION AG183488.1 GI:16713168  
 KEYWORDS GSS.

## SOURCE

ORGANISM Pan troglodytes male lymphocytes DNA, clone\_lib:RPCI-43 Chimpanzee  
 Male BAC Library clone:RP43-056P19.TJ.

## REFERENCE

AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
 Totoki,Y., Watanabe,H. and Sakaki,Y.

## TITLE

BAC end sequences of Library RPCI-43

Unpublished

2 (bases 1 to 689)

## REFERENCE

AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
 Totoki,Y., Watanabe,H. and Sakaki,Y.

## TITLE

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
 1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 (E-mail:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,  
 Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library RPCI-43. This BAC  
 end was generated during the R&D process and may have higher chance  
 of clone tracking errors.

## PRIMERS

Sequencing: TJ

## LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

## FEATURES

## source

Location/Qualifiers  
 1..689  
 /organism="Pan troglodytes"  
 /db\_xref="taxon:9598"  
 /clone="RP43-056P19.TJ"  
 /sex="male"  
 /cell\_type="lymphocytes"  
 /clone\_lib="RPCI-43 Chimpanzee Male BAC Library"

BASE COUNT 196 a 148 c 103 g 242 t

## ORIGIN

Query Match 8.3%; Score 82.8; DB 17; Length 689;  
 Best Local Similarity 65.4%; Pred. No. 2.3e-07;  
 Matches 170; Conservative 0; Mismatches 82; Indels 8; Gaps 3;



Db 308 GGTGGCCATGTACAAGCCTTANGACAGAGGCTTCGGGAGGAGCAACCCAGCCACACCTT 367  
Qy 419 GATGTTGGACTTC 431  
Db 368 GATTCAGACTTC 380

Search completed: December 24, 2002, 21:53:54  
Job time : 1117.8 secs

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